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(54) Title: GENE EXPRESSION PROFILES IN NORMAL AND CANCER CELLS

(57) Abstract

As a step towards understanding the complex differences between normal and cancer cells, gene expression patterns were examined in gastrointestinal tumors. More than 300,000 transcripts derived from at least 45,000 different genes were analyzed. Although extensive similarity was noted between the expression profiles, more than 500 transcripts that were expressed at significantly different levels in normal and neoplastic cells were identified. These data provide insights into the extent of expression differences underlying malignancy and reveal genes that are useful as diagnostic or prognostic markers.

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# Gene Expression Profiles in Normal and Cancer Cells

This invention was made with support from the National Institutes of Health, Grant No. GM07309, CA57345, and CA62924. The U.S. government therefore retains certain rights in the invention.

## TECHNICAL FIELD OF THE INVENTION

This invention is related to the diagnosis of cancer, and tools for carrying out such diagnosis.

## BACKGROUND OF THE INVENTION

Much of cancer research over the past 50 years has been devoted to the analyses of genes that are expressed differently in tumor cells compared to their normal counterparts. Although hundreds of studies have pointed out differences in the expression of one or a few genes, no comprehensive study of gene expression in the cancer cell has been reported. It is therefore not known how many genes are expressed differentially in tumor versus normal cells, whether the bulk of these differences are cell autonomous rather than being dependent on the tumor microenvironment, and whether most differences are cell-type specific or tumor specific. Thus there is a need in the art for information on the molecular changes that occur in cells during cancer development and progression.

## SUMMARY OF THE INVENTION

According to one embodiment of the invention, a method is provided for diagnosing colon cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be lower in the first sample than in the second sample.

According to another embodiment of the invention, another method is provided for diagnosing colon cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

In another embodiment of the invention an isolated and purified human nucleic acid molecule is provided. The molecule comprises a SAGE tag selected from SEQ ID NO:1-732.

In yet another aspect of the invention an isolated nucleotide probe is provided. The probe comprises at least 12 nucleotides of a human nucleic acid molecule, wherein the human nucleic acid molecule comprises a SAGE tag selected from SEQ ID NO: 1-732.

According to another aspect of the invention a method is provided for diagnosing pancreatic cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

According to still another embodiment of the invention a method of diagnosing cancer in a sample suspected of being neoplastic is provided. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

According to another embodiment of the invention a method is provided to aid in the determination of a prognosis for a colon cancer patient. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of the at least one transcript is found to be lower in the first sample than in the second sample.

According to another aspect of the invention a method to aid in determining a prognosis for a patient with colon cancer is provided. The method comprises the steps of:

comparing the level of at least one transcript in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

In yet another embodiment of the invention a method is provided for diagnosing colon cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

identifying the first sample as neoplastic when the level of expression of the protein is found to be lower in the first sample than in the second sample.

In another aspect of the invention a method of diagnosing colon cancer in a sample suspected of being neoplastic is provided. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript

identified by a tag selected from the group consisting of those shown in Table 2;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

According to another embodiment of the invention a method is provided to aid in determining a prognosis of a patient having pancreatic cancer. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

determining a poorer prognosis if transcription is found to be higher in the first sample than in the second sample.

In yet another aspect of the invention a method to aid in providing a prognosis for a cancer patient is provided. The method comprises the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

determining a poorer prognosis if transcription is found to be higher in the first sample than in the second sample.

According to still another aspect of the invention, a method is provided for diagnosing pancreatic cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of expression of at least one protein encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said protein is

encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

According to yet another aspect of the invention a method is provided for diagnosing cancer in a sample suspected of being neoplastic. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

In still another embodiment of the invention a method is provided to aid in the determination of a prognosis of a colon cancer patient. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of expression is found to be lower in the first sample than in the second sample.

In still another embodiment of the invention a method is provided to aid in determining a prognosis for a patient with colon cancer. The method comprises the steps of:

comparing the level of expression of at least one protein in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and

wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

In still another aspect of the invention a method is provided to aid in determining a prognosis of a patient having pancreatic cancer. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

According to even a further aspect of the invention a method is provided to aid in providing a prognosis for a cancer patient. The method comprises the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

In still another embodiment of the invention a method of treating a cancer cell is provided. The method comprises the step of:

administering to a cancer cell an antibody which specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5, wherein the antibody is linked to a cytotoxic agent.

In another aspect of the invention an antibody linked to a cytotoxic agent is provided. The antibody specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5.

According to another aspect of the invention, a method of detecting colon cancer in a patient is provided. The method comprises the steps of:

comparing the level of at least one protein or transcript in a first body sample to a second body sample, wherein the first sample is a body sample of the patient and the second sample is of a normal human, wherein the protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

In another aspect of the invention a method of detecting pancreatic cancer in a patient is provided. The method comprises the steps of:

comparing the level of at least one protein or transcript encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of the patient and the second sample is of a normal human, wherein said protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

Also provided by the present invention is a method of detecting cancer in a patient. The method comprises the steps of:

comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of patient and the second sample is of a normal human, wherein said protein is encoded by a

transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

Additionally provided by the present invention is a method to aid in the determination of a prognosis for a colon cancer patient. The method comprises the steps of:

comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a colon cancer patient and the second sample is of a normal human, wherein the protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown in Table 3, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be lower in the first sample than in the second sample.

Provided by another embodiment of the invention is a method to aid in determining a prognosis for a patient with colon cancer. The method comprises the steps of:

comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a colonic cancer patient and the second sample is of a normal human, wherein the protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

According to still another aspect of the invention, a method to aid in determining a prognosis of a patient having pancreatic cancer is provided. The method comprises the steps of:

comparing the level of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a pancreatic cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein said first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

Also provided by the present invention is a method to aid in providing a prognosis for a cancer patient. The method comprises the steps of:

comparing the level of expression of at least one protein or transcript in a first sample to a second sample, wherein the first sample is of a cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript and the transcript is identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein or transcript is found to be higher in the first sample than in the second sample.

The present invention further includes antisense oligonucleotides complementary in whole or in part to SEQ ID NOS:1-732.

This invention also provides a method for screening for candidate agents that modulate the expression of a polynuleotide selected from the group consisting of the polynucleotides in SEQ ID NOS.1-732 or their respective complements, by contacting a test agent with a pancreatic or colon cell and monitoring expression of the polynucleotide, wherein the test agent which modifies the expression of the polynucleotide is a candidate agent.

The present invention provides the art with new methods and reagents for diagnosing and prognosing cancers. In addition, some of the newly disclosed genes may play an important role in the development of cancers.

## BRIEF DESCRIPTION OF THE DRAWINGS

**Fig. 1.** Comparison of expression patterns in colorectal cancers and normal colon epithelium. **(FIG. 1A)** A semi-logarithmic plot reveals 51 tags that were decreased more than 10 fold in primary CR cancer cells whereas 32 tags were increased more than 10 fold. 62,168 and 60,878 tags derived from normal colon epithelium and primary CR cancers, respectively, were used for this analysis. The relative expression of each transcript was determined by dividing the number of tags observed in tumor and normal tissue as indicated. To avoid division by 0, a tag value of 1 was used for any tag that was not detectable in one of the samples. These ratios were then rounded to the nearest integer and their distribution plotted on the abscissa. The number of genes displaying each ratio was plotted on the ordinate. Tu: CR tumors; NC: Normal colon. **(FIG. 1B** and **FIG. 1C)** Differentially expressed genes in colorectal cancers. The number of transcripts found to be differentially expressed ($P < 0.01$) are presented as Venn diagrams. Diagrams of transcripts that were decreased **(FIG. 1B)** or increased **(FIG. 1C)** in CR cancers compared to normal colon epithelium. Comparisons were between primary tumors and cells in culture as indicated.

**Fig. 2.** Northern blot analysis of genes differentially expressed in gastrointestinal neoplasia. Northern blot analysis was performed on total RNA (5 µg isolated from primary CR carcinomas (T) and matching normal colon epithelium (N), or pancreatic carcinomas. The top panel in each case show an

example of the ethidium bromide stained gels prior to transfer. The number of SAGE tags observed in the original analysis is indicated to the right of each blot. (**FIG. 2A**) Examples of transcripts that were decreased or increased in CR cancers. (**FIG.2B**) Examples of transcripts increased in pancreatic cancers (*10*). (**FIG.2C**) Examples of transcripts elevated in cancer which were or were not cancer type specific. Probes used for Northern blot analysis were as follows (Human SAGE Tag unique identifier, gene name, (GenBank accession number)): (**FIG. 2A**) H204104, Guanylin (M95714); H259108, (see Table 2); H1000193, (see Table 2); H998030, (see Table 2). (**FIG. 2B**) H294155, RIG-E (U42376); H560056, TIMP-1 (S68252). (**FIG. 2C**) H802810, EST338411 (W52120); H85882, 1-8D (X57351); H618841, GA733-1 (X13425).

**Tables 2-5.** Transcripts Differentially Expressed in Human Cancer.

Tag sequence represents the NlaIII site plus the adjacent 11 bp SAGE tag. Tag number indicates a SAGE UID (unique identifier). NC, TU, CL, PT, PC, refers to the number of the indicated tag observed in RNA isolated from normal colorectal epithelium, primary colorectal cancers, colorectal cancer cell lines, primary pancreatic cancers, or pancreatic cancer cell lines, respectively. The Accession and Gene Name refer to representative GenBank entries that contain the tag sequence.

Table 2 Transcripts increased in colorectal cancer.

Table 3 Transcripts decreased in colorectal cancer.

Table 4 Transcripts increased in pancreatic cancer.

Table 5 Transcripts increased in pancreatic and colorectal cancer.

## DETAILED DESCRIPTION

The inventors have discovered sets of human genes which are either upregulated or downregulated in cancer cells, as compared to normal cells. Specifically, certain genes have been found to be upregulated or downregulated in colorectal and/or pancreatic cancer cells, when compared to normal colon

cells. These sets of differentially regulated genes can be used as diagnostic markers, either individually or in sets of, for example, 2, 5, 10, 20, or 30.

Genes whose expression was detected to be increased in colorectal cancer are shown in Table 2. Genes whose expression was detected to be decreased in colorectal cancer are shown in Table 3. Genes whose expression was detected as increased in pancreatic cancer are shown in Table 4. Genes whose expression was detected as increased in both pancreatic cancer and colorectal cancer are shown in Table 5. These latter genes likely play a role in neoplastic development generally.

Tag sequences, as provided herein, uniquely identify genes. This is due to their length, and their specific location (3') in a gene from which they are drawn. The full length genes can be identified by matching the tag to a gene data base member, or by using the tag sequences as probes to physically isolate previously unidentified genes from cDNA libraries. The methods by which genes are isolated from libraries using DNA probes are well known in the art. See, for example, Veculescu et al., Science 270: 484 (1995), and Sambrook et al. (1989), MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed. (Cold Spring Harbor Press, Cold Spring Harbor, New York). Once a gene or transcript has been identified, either by matching to a data base entry, or by physically hybridizing to a cDNA molecule, the position of the hybridizing or matching region in the transcript can be determined. If the tag sequence is not in the 3' end, immediately adjacent to the restriction enzyme used to generate the SAGE tags, then a spurious match may have been made. Confirmation of the identity of a SAGE tag can be made by comparing transcription levels of the tag to that of the identified gene in certain cell types.

In addition to the sequences shown in SEQ ID NOS: 1-732, or their complements, this invention also provides the anti-sense polynucleotide stand, e.g. antisense RNA to these sequences or their complements. One can obtain an antisense RNA using the sequences provided in SEQ ID NOS: 1-732 and the methodology described in Vander Krol et al. (1988) BioTechniques 6:958.

The invention also encompasses polynucleotides which differ from that of the polynucleotides described above, but which produce the same phenotypic effect, such as the allele. These altered, but phenotypically equivalent polynucleotides are referred to "equivalent nucleic acids." This invention also encompasses polynucleotides characterized by changes in non-coding regions that do not alter the phenotype of the polypeptide produced therefrom when compared to the polynucleotide herein. This invention further encompasses polynucleotides, which hybridize to the polynucleotides of the subject invention under conditions of moderate or high stringency.

The polynucleotides can be conjugated to a detectable marker, e.g., an enzymatic label or a radioisotope for detection of nucleic acid and/or expression of the gene in a cell. A wide variety of appropriate detectable markers are known in the art, including fluorescent, radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred embodiments, one will likely desire to employ a fluorescent label or an enzyme tag, such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with complementary nucleic acid-containing samples. Briefly, this invention further provides a method for detecting a single-stranded polynucleotide identified by SEQ ID NOS.1-732 or its complement, by contacting target single-stranded polynucleotides with a labeled, single-stranded polynucleotide (a probe) which is at least 10 nucleotides of the complement of SEQ ID NOS: 1-732 (or the corresponding complement) under conditions permitting hybridization (preferably moderately stringent hybridization conditions) of complementary single-stranded polynucleotides, or more preferably, under highly stringent hybridization conditions. Hybridized polynucleotide pairs are separated from un-hybridized, single-stranded polynucleotides. The hybridized polynucleotide

pairs are detected using methods well known to those of skill in the art and set forth, for example, in Sambrook et al. (1989) supra.

The polynucleotides of this invention can be isolated using the technique described in the experimental section or replicated using PCR. The PCR technology is the subject matter of United States Patent Nos.4,683,195, 4,800,159, 4,754,065, and 4,683,202 and described in PCR: The Polymerase Chain Reaction (Mullis et al. eds, Birkhauser Press, Boston (1994)) or MacPherson et al. (1991) and (1994), supra, and references cited therein. Alternatively, one of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to replicate the DNA. Accordingly, this invention also provides a process for obtaining the polynucleotides of this invention by providing the linear sequence of the polynucleotide, nucleotides, appropriate primer molecules, chemicals such as enzymes and instructions for their replication and chemically replicating or linking the nucleotides in the proper orientation to obtain the polynucleotides. In a separate embodiment, these polynucleotides are further isolated. Still further, one of skill in the art can insert the polynucleotide into a suitable replication vector and insert the vector into a suitable host cell (procaryotic or eucaryotic) for replication and amplification. The DNA so amplified can be isolated from the cell by methods well known to those of skill in the art. A process for obtaining polynucleotides by this method is further provided herein as well as the polynucleotides so obtained.

RNA can be obtained by first inserting a DNA polynucleotide into a suitable host cell. The DNA can be inserted by any appropriate method, e.g., by the use of an appropriate gene delivery vector or by electroporation. When the cell replicates and the DNA is transcribed into RNA; the RNA can then be isolated using methods well known to those of skill in the art, for example, as set forth in Sambrook et al. (1989) supra. For instance, mRNA can be isolated using various lytic enzymes or chemical solutions according to the procedures set forth in Sambrook et al. (1989), supra or extracted by nucleic-acid-binding resins following the accompanying instructions provided by manufactures.

Polynucleotides having at least 10 nucleotides and exhibiting sequence complementarity or homology to SEQ ID NOS: 1-732 find utility as hybridization probes. In some aspects, the full coding sequence of the transcript, i.e., for SEQ ID NOS: 1-732, are known. Accordingly, any portion of the known sequences available in GenBank, or homologous sequences, can be used in the methods of this invention.

It is known in the art that a "perfectly matched" probe is not needed for a specific hybridization. Minor changes in probe sequence achieved by substitution, deletion or insertion of a small number of bases do not affect the hybridization specificity. In general, as much as 20% base-pair mismatch (when optimally aligned) can be tolerated. Preferably, a probe useful for detecting the aforementioned mRNA is at least about 80% identical to the homologous region of comparable size contained in the previously identified sequences identified by SEQ ID NOS:1-732, which correspond to previously characterized genes or SEQ ID NOS:1-732, which correspond to known ESTs. More preferably, the probe is 85% identical to the corresponding gene sequence after alignment of the homologous region; even more preferably, it exhibits 90% identity.

These probes can be used in radioassays (e.g. Southern and Northern blot analysis) to detect, prognose, diagnose or monitor various pancreatic or colon cells or tissue containing these cells. The probes also can be attached to a solid support or an array such as a chip for use in high throughput screening assays for the detection of expression of the gene corresponding to one or more polynucleotide(s) of this invention. Accordingly, this invention also provides at least one of the transcripts identified as SEQ ID NOS:1-732, or its complement, attached to a solid support for use in high throughput screens.

The total size of fragment, as well as the size of the complementary stretches, will depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the complementary region may be varied,

such as between about 10 and about 100 nucleotides, or even full length according to the complementary sequences one wishes to detect.

Nucleotide probes having complementary sequences over stretches greater than 10 nucleotides in length are generally preferred, so as to increase stability and selectivity of the hybrid, and thereby improving the specificity of particular hybrid molecules obtained. More preferably, one can design polynucleotides having gene-complementary stretches of more than 50 nucleotides in length, or even longer where desired. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCR technology with two priming oligonucleotides as described in U.S. Pat. No. 4,603,102 or by introducing selected sequences into recombinant vectors for recombinant production. A preferred probe is about 50-75 or more preferably, 50-100, nucleotides in length.

The polynucleotides of the present invention can serve as primers for the detection of genes or gene transcripts that are expressed in pancreatic or colon cells. In this context, amplification means any method employing a primer-dependent polymerase capable of replicating a target sequence with reasonable fidelity. Amplification may be carried out by natural or recombinant DNA-polymerases such as T7 DNA polymerase, Klenow fragment of E.coli DNA polymerase, and reverse transcriptase.

A preferred amplification method is PCR. However, PCR conditions used for each reaction are empirically determined. A number of parameters influence the success of a reaction. Among them are annealing temperature and time, extension time, $Mg^{2+}$ ATP concentration, pH, and the relative concentration of primers, templates, and deoxyribonucleotides. After amplification, the resulting DNA fragments can be detected by agarose gel electrophoresis followed by visualization with ethidium bromide staining and ultraviolet illumination.

The invention further provides the isolated polynucleotide operatively linked to a promoter of RNA transcription, as well as other regulatory

sequences for replication and/or transient or stable expression of the DNA or RNA. As used herein, the term "operatively linked" means positioned in such a manner that the promoter will direct transcription of RNA off the DNA molecule. Examples of such promoters are SP6, T4 and T7. In certain embodiments, cell-specific promoters are used for cell-specific expression of the inserted polynucleotide. Vectors which contain a promoter or a promoter/enhancer, with termination codons and selectable marker sequences, as well as a cloning site into which an inserted piece of DNA can be operatively linked to that promoter are well known in the art and commercially available. For general methodology and cloning strategies, see Gene Expression Technology (Goeddel ed., Academic Press, Inc. (1991)) and references cited therein and Vectors: Essential Data Series (Gacesa and Ramji, eds., John Wiley & Sons, N.Y. (1994)), which contains maps, functional properties, commercial suppliers and a reference to GenEMBL accession numbers for various suitable vectors. Preferable, these vectors are capable of transcribing RNA in vitro or in vivo.

Fragment of the sequences shown in SEQ ID NOS:1-732 or their respective complements also are encompassed by this invention, preferably at least 10 nucleotides and more preferably having at least 18 nucleotides. Larger polynucleotides, e.g., cDNA or genomic DNA, which hybridize under moderate or stringent conditions to the polynucleotide sequences shown in SEQ ID NOS:1-732, or their respective complements, also are encompassed by this invention.

In one embodiment, these fragments are polynucleotides that encode polypeptides or proteins having diagnostic and therapeutic utilities as described herein as well as probes to identify transcripts of the protein which may or may not be present. These nucleic acid fragments can by prepared, for example, by restriction enzyme digestion of the polynucleotide of SEQ ID NOS:1-732, or their complements, and then labeled with a detectable marker. Alternatively, random fragments can be generated using nick translation of the molecule. For

methodology for the preparation and labeling of such fragments, see Sambrook et al., (1989) supra.

Expression vectors containing these nucleic acids are useful to obtain host vector systems to produce proteins and polypeptides. It is implied that these expression vectors must be replicable in the host organisms either as episomes or as an integral part of the chromosomal DNA. Suitable expression vectors include viral vectors, including adenoviruses, adeno-associated viruses, retroviruses, cosmids, etc. Adenoviral vectors are particularly useful for introducing genes into tissues in vivo because of their high levels of expression and efficient transformation of cells both in vitro and in vivo. When a nucleic acid is inserted into a suitable host cell, e.g., a procaryotic or a eucaryotic cell and the host cell replicates, the protein can be recombinantly produced. Suitable host cells will depend on the vector and can include mammalian cells, animal cells, human cells, simian cells, insect cells, yeast cells, and bacterial cells constructed using well known methods. See Sambrook et al. (1989) supra. In addition to the use of viral vector for insertion of exogenous nucleic acid into cells, the nucleic acid can be inserted into the host cell by methods well known in the art such as transformation for bacterial cells; transfection using calcium phosphate precipitation for mammalian cells; or DEAE-dextran; electroporation; or microinjection. See Sambrook et al. (1989) supra for this methodology. Thus, this invention also provides a host cell, e.g. a mammalian cell, an animal cell (rat or mouse), a human cell, or a procaryotic cell such as a bacterial cell, containing a polynucleotide encoding a protein or polypeptide or antibody.

When the vectors are used for gene therapy *in vivo* or *ex vivo*, a pharmaceutically acceptable vector is preferred, such as a replication-incompetent retroviral or adenoviral vector. Pharmaceutically acceptable vectors containing the nucleic acids of this invention can be further modified for transient or stable expression of the inserted polynucleotide. As used herein, the term "pharmaceutically acceptable vector" includes, but is not limited to, a vector or delivery vehicle having the ability to selectively target

and introduce the nucleic acid into dividing cells. An example of such a vector is a "replication-incompetent" vector defined by its inability to produce viral proteins, precluding spread of the vector in the infected host cell. An example of a replication-incompetent retroviral vector is LNL6 (Miller, A.D. et al. (1989) BioTechniques 7:980-990). The methodology of using replication-incompetent retroviruses for retroviral-mediated gene transfer of gene markers is well established (Correll et al. (1989) PNAS USA 86:8912; Bordignon (1989) PNAS USA 86:8912-52; Culver, K. (1991) PNAS USA 88:3155; and Rill, D.R. (1991) Blood 79(10):2694-700. Clinical investigations have shown that there are few or no adverse effects associated with the viral vectors, see Anderson (1992) Science 256:808-13.

Compositions containing the polynucleotides of this invention, in isolated form or contained within a vector or host cell are further provided herein. When these compositions are to be used pharmaceutically, they are combined with a pharmaceutically acceptable carrier.

This invention further encompasses genes, either genomic or cDNA, which code for a polypeptide or protein in the cell of interest. The genes specifically hybridize under moderate or stringent conditions to a polynucleotide identified by SEQ ID NOS: 1-732 or their respective complements. The process of identification of larger fragment or the full-length coding sequence to which the partial sequence depicted in SEQ ID NOS:1-732 hybridizes preferably involves the use of the methods and reagents provided in this invention, either singularly or in combination.

Five methods are disclosed herein which allows one of skill in the art to isolate the gene or cDNA corresponding to the transcripts of the invention.

RACE-PCR Technique

One method to isolate the gene or cDNA which code for a polypeptide or protein and which corresponds to a transcript of this invention, involves the 5'-RACE-PCR technique. In this technique, the poly-A mRNA that contains the coding sequence of particular interest is first identified by hybridization to

a sequence disclosed herein and then reverse transcribed with a 3'-primer comprising the sequence disclosed herein. The newly synthesized cDNA strand is then tagged with an anchor primer of a known sequence, which preferably contains a convenient cloning restriction site attached at the 5'end. The tagged cDNA is then amplified with the 3'-primer (or a nested primer sharing sequence homology to the internal sequences of the coding region) and the 5'-anchor primer. The amplification may be conducted under conditions of various levels of stringency to optimize the amplification specificity. 5'-RACE-PCR can be readily performed using commercial kits (available from, e.g., BRL Life Technologies Inc, Clotech) according to the manufacturer's instructions.

Identification of known genes or ESTs

In addition, databases exist that reduce the complexity of ESTs by assembling contiguous EST sequences into tentative genes. For example, TIGR has assembled human ESTs into a datable called THC for tentative human consensus sequences. The THC database allows for a more definitive assignment compared to ESTs alone. Software programs exist (give examples) that allow for assembling ESTs into contiguous sequences from any organism.

Isolation of cDNAs from a library by probing with the SAGE transcript or tag

Alternatively, mRNA from a sample preparation was used to construct cDNA library in the ZAP Express vector following the procedure described in Velculescu et al. (1997) Science 270:484. The ZAP Express cDNA synthesis kit (Stratagene) was used accordingly to the manufacturer's protocol. Plates containing 250 to 2000 plaques are hybridized as described in Rupert et al. (1988) Mol. Cell. Bio. 8:3104 to oligonucleotide probes with the same conditions previously described for standard probes exxcept that the hybridization temperature is reduced to room temperature. Washes are performed in 6X standard-saline-citrate 0.1% SDS for 30 minutes at room temperature. The probes are labeled with 32P-ATP through use of T4 polynucletoide kinase.

Table 2 - Transcripts increased in colon cancer

## Transcripts increased in only colon primary tumors compared to normal colon (61 genes)

NC: Normal Colon
TU: Colon Primary Tumor
CL: Colon Cancer Cell Line
PT: Pancreatic Primary Tumor
PC: Pancreatic Cancer Cell Line

| # | Tag Sequence | Tag_Number | NC | TU | CL | PT | PC | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGCACCTAATTGG | H285759 | 612 | 755 | 411 | 161 | 333 | F15516 | H.sapiens mitochondrial EST sequence (1-t-12) from |
| 2 | CATGTGATTTCACTT | H933704 | 452 | 595 | 235 | 80 | 314 | U35430 | Human cytochrome c oxidase subunit III (COIII) pse |
| 3 | CATGCCTGTAATCCC | H388150 | 433 | 549 | 380 | 443 | 197 | Z70701 | H.sapiens mRNA (fetal brain cDNA c2_11). |
| | | | | | | | | X71347 | H.sapiens HNF1-C mRNA. |
| | | | | | | | | X71346 | H.sapiens HNF1-B mRNA. |
| 4 | CATGCACTACTCACC | H291282 | 293 | 527 | 78 | 14 | 83 | U09500 | Human mitochondrion cytochrome b gene, partial cds |
| 5 | CATGGTGAAACCCCA(G) | H753750 | 392 | 517 | 389 | 453 | 194 | X66785 | H.sapiens mRNA for transacylase (DBT). |
| | | | | | | | | X17648 | Human mRNA for granulocyte-macrophage colony-stimu |
| | | | | | | | | U09087 | Human thymopoietin beta mRNA, complete cds. |
| | | | | | | | | U09088 | Human thymopoietin gamma mRNA, complete cds. |
| | | | | | | | | U20770 | Human metastasis suppressor (KAI1) mRNA, complete |
| 6 | CATGGGCTTTAGGGA | H687915 | 37 | 372 | 6 | 29 | 11 | W15552 | zb91h11.s1 Soares parathyroid tumor NbHPA Homo sap |
| | | | | | | | | W32091 | zc05d03.s1 Soares parathyroid tumor NbHPA Homo sap |
| | | | | | | | | R62866 | yi11d07.r1 Homo sapiens cDNA clone 138925 5'. |
| 7 | CATGACTTTCCAAA | H130369 | 32 | 272 | 32 | 23 | 20 | X89839 | H.sapiens mitochondrial DNA for loop attachment se |
| 8 | CATGTGGTGTATGCA | H965434 | 53 | 271 | 6 | 30 | 5 | T11555 | A1486F Homo sapiens cDNA clone A1486 similar to Mi |
| 9 | CATGAGGGTGTTTTC | H175872 | 26 | 218 | 7 | 20 | 10 | T15773 | IB1870 Homo sapiens cDNA 3'end similar to Human mi |
| 10 | CATGAGGTCAGGAGA(T) | H177315 | 93 | 213 | 113 | 148 | 58 | X12544 | Human mRNA for HLA class II DR-beta (HLA-DR B). |
| | | | | | | | | S73483 | phosphorylase kinase catalytic subunit PHKG2 homol |
| 11 | CATGTTGGCCAGGCT | H1025322 | 124 | 194 | 63 | 111 | 51 | X74301 | H.sapiens mRNA for MHC class II transactivator. |
| | | | | | | | | U28687 | Human zinc finger containing protein ZNF157 (ZNF15 |
| | | | | | | | | U29119 | Human leiomyoma LM-196.4 ectopic sequence from HMG |
| | | | | | | | | U56236 | Human Fc alpha receptor b mRNA, complete cds. |
| 12 | CATGATCACGCCCTC | H214616 | 97 | 186 | 17 | 41 | 49 | W03751 | za62h11.r1 Soares fetal liver spleen 1NFLS Homo sa |
| | | | | | | | | W03770 | za63f10.r1 Soares fetal liver spleen 1NFLS Homo sa |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | W04748 | za42f09.r1 Soares fetal liver spleen 1NFLS Homo sa |
| 13 | CATGGGGGTCAGGGG | H699691 | 37 | 170 | 11 | 16 | 9 | T12078 | A730R Homo sapiens cDNA clone A730 similar to Mito |
| | | | | | | | | W45641 | zc26a12.s1 Soares senescent fibroblasts NbHSF Homo |
| 14 | CATGGCTAGGTTTAT | H641789 | 38 | 144 | 13 | 25 | 13 | D51017 | Human fetal brain cDNA 3'-end GEN-007C04. |
| | | | | | | | | D53694 | Human fetal brain cDNA 3'-end GEN-117E01. |
| 15 | CATGCCCCGTACATC | H350996 | 56 | 132 | 35 | 0 | 18 | | Unknown |
| 16 | CATGAGTAGGTGGCC | H183018 | 18 | 131 | 2 | 17 | 7 | D51021 | Human fetal brain cDNA 3'-end GEN-007D07. |
| | | | | | | | | D51052 | Human fetal brain cDNA 3'-end GEN-009C05. |
| | | | | | | | | D52836 | Human fetal brain cDNA 3'-end GEN-089E01. |
| 17 | CATGCCTGTAGTCCC | H388278 | 79 | 124 | 61 | 71 | 23 | D83195 | Human DNA for Deoxyribonuclease I precursor. |
| 18 | CATGAGACCCACAAC | H136465 | 64 | 121 | 28 | 24 | 15 | D54113 | Human fetal brain cDNA 5'-end GEN-129B05. |
| 19 | CATGCATTTGTAATA | H327364 | 49 | 107 | 35 | 7 | 40 | F15796 | H.sapiens mitochondrial EST sequence (102-25) from |
| 20 | CATGTCCCCGTACCT | H874182 | 28 | 78 | 14 | 0 | 13 | | |
| 21 | CATGGCCAACCTCCT | H606582 | 23 | 73 | 8 | 6 | 19 | Z59183 | H.sapiens CpG island DNA genomic Mse1 fragment, cl |
| | | | | | | | | D52905 | Human fetal brain cDNA 5'-end GEN-091D11. |
| 22 | CATGGCCATCCCCTT | H609624 | 29 | 73 | 7 | 14 | 16 | F16449 | H.sapiens mitochondrial EST sequence (129-09) from |
| 23 | CATGTTGGTCAGGCT | H1027370 | 35 | 67 | 18 | 35 | 14 | U06452 | Human melanoma antigen recognized by T-cells (MART |
| 24 | CATGTCCTATTAAG | H881603 | 20 | 49 | 17 | 15 | 26 | | |
| 25 | CATGTTACTTATACT | H991026 | 2 | 47 | 2 | 1 | 4 | D51004 | Human fetal brain cDNA 3'-end GEN-006D02. |
| | | | | | | | | L49057 | Homo sapiens retinal fovea EST HFD010904 sequence. |
| | | | | | | | | D51071 | Human fetal brain cDNA 3'-end GEN-010E01. |
| 26 | CATGATGGCAGGAGT | H238755 | 13 | 45 | 1 | 4 | 2 | | |
| 27 | CATGCTAAGGCGAGG | H461411 | 5 | 44 | 2 | 3 | 3 | | |
| 28 | CATGGGTGAGACACT | H713234 | 7 | 44 | 20 | 13 | 15 | J03592 | Human ADP/ATP translocase mRNA, 3' end, clone pHAT |
| 29 | CATGACCTGTATCCC | H97078 | 6 | 42 | 17 | 100 | 32 | X57352 | Human 1-8U gene from interferon-inducible gene fam |
| 30 | CATGCCAGTCCGCCT | H339302 | 0 | 39 | 0 | 1 | 0 | H01571 | yj33e06.r1 Homo sapiens cDNA clone 150562 5' simil |
| | | | | | | | | H03072 | yj46g12.r1 Homo sapiens cDNA clone 151846 5' simil |
| 31 | CATGTAATTTTTGCC | H802810 | 1 | 37 | 0 | 1 | 0 | T25155 | EST730 Homo sapiens cDNA clone 34C11. |
| 32 | CATGTTAGCTTGTTT | H993264 | 6 | 37 | 2 | 3 | 5 | D50972 | Human fetal brain cDNA 3'-end GEN-004A05. |
| | | | | | | | | D51211 | Human fetal brain cDNA 3'-end GEN-017E08. |
| | | | | | | | | D52162 | Human fetal brain cDNA 3'-end GEN-069F04. |
| | | | | | | | | T23865 | seq2012 Homo sapiens cDNA clone Cot1374Ft-4HB3MA-3 |
| 33 | CATGGCCACCCCCTG | H607576 | 0 | 35 | 1 | 0 | 0 | M32053 | Human H19 RNA gene, complete cds. |
| 34 | CATGTAATAAAGGTG | H798764 | 13 | 35 | 19 | 33 | 51 | X67247 | H.sapiens rpS8 gene for ribosomal protein S8. |
| 35 | CATGTACTGCTCGGA | H817627 | 13 | 35 | 5 | 1 | 14 | T11939 | A953F Homo sapiens cDNA clone A953 similar to Mito |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 36 | CATGGTGAAACCCA | H753749 | 9 | 31 | 22 | 30 | 4 | T95857 | ye42f01.s1 Homo sapiens cDNA clone 120409 3' simil |
| | | | | | | | | W03237 | za35b09.r1 Soares fetal liver spleen 1NFLS Homo sa |
| | | | | | | | | W03326 | za63g03.r1 Soares fetal liver spleen 1NFLS Homo sa |
| 37 | CATGGAAACTGAACA | H526210 | 6 | 26 | 17 | 5 | 3 | X54195 | Human line-1 element DNA, host sequence flanking t |
| | | | | | | | | U29607 | Human methionine aminopeptidase mRNA, complete cds |
| | | | | | | | | H95100 | yw57b10.r1 Homo sapiens cDNA clone 256315 5' simil |
| 38 | CATGACTTTTTAAAA | H131009 | 1 | 22 | 4 | 1 | 0 | | |
| 39 | CATGGACTGCGTGCC | H555450 | 0 | 21 | 7 | 9 | 12 | D29062 | Human keratinocyte cDNA, clone 067. |
| | | | | | | | | D29563 | Human keratinocyte cDNA, clone 713. |
| 40 | CATGTCAGTGGTAGT | H863923 | 4 | 21 | 2 | 2 | 1 | T03196 | FB3B5 Homo sapiens cDNA clone FB3B5 3'end. |
| 41 | CATGAAACTGTGGTT | H7916 | 2 | 20 | 2 | 2 | 1 | Z57093 | H.sapiens CpG DNA, clone 164a10; reverse read cpg1 |
| | | | | | | | | Z60184 | H.sapiens CpG island DNA genomic Mse1 fragment, cl |
| | | | | | | | | Z63649 | H.sapiens CpG island DNA genomic Mse1 fragment, cl |
| | | | | | | | | W31349 | zb95d06.s1 Soares parathyroid tumor NbHPA Homo sap |
| 42 | CATGGGGGGGGGGT | H699051 | 0 | 19 | 0 | 0 | 0 | | |
| 43 | CATGGTGCCCGTGCC | | 2 | 19 | 1 | 0 | 0 | W31448 | zb96h01.s1 Soares parathyroid tumor NbHPA Homo sap |
| | | | | | | | | W47282 | zc40b06.r1 Soares senescent fibroblasts NbHSF Homo |
| 44 | CATGGGGGGTAACTA | H699144 | 3 | 19 | 15 | 12 | 5 | X71428 | H.sapiens fus mRNA. |
| | | | | | | | | S62140 | TLS=translocated in liposarcoma [human, mRNA, 1824 |
| | | | | | | | | W31782 | zb96a06.r1 Soares parathyroid tumor NbHPA Homo sap |
| 45 | CATGTCCTGCCCCAT | H883029 | 3 | 19 | 14 | 27 | 16 | M24398 | Human parathymosin mRNA, complete cds. |
| 46 | CATGAAGTGGCAAGA | H47683 | 0 | 16 | 0 | 0 | 0 | | |
| 47 | CATGGGTATTAACCA | H708358 | 0 | 16 | 0 | 0 | 0 | U33317 | Human defensin 6 (HD-6) gene, complete cds. |
| | | | | | | | | M98331 | Homo sapiens defensin 6 mRNA, complete cds. |
| 48 | CATGGGCTACACCTT | H684312 | 2 | 16 | 0 | 2 | 1 | D32027 | Human mRNA for T cell receptor V beta 14 CDR3, par |
| | | | 2 | 16 | 0 | 2 | 1 | T11701 | A1225F Homo sapiens cDNA clone A1225 similar to Mi |
| 49 | CATGAGGGTGTTTCC | H175870 | 1 | 15 | 0 | 0 | 0 | D51783 | Human fetal brain cDNA 5'-end GEN-051G02. |
| 50 | CATGCAAGGACCAGC | H272467 | 0 | 13 | 0 | 2 | 0 | D13138 | Human mRNA for dipeptidase. |
| | | | | | | | | | Homo sapiens (clones MDP4, MDP7) microsomal dipept |
| | | | | | | | | | RDP=renal dipeptidase [human, kidney, Genomic, 357 |
| 51 | CATGTGGAAATGACC | H950498 | 0 | 13 | 0 | 167 | 0 | M10629 | Human alpha-1 collagen gene, 3' end with polyA sit |
| 52 | CATGATCCGCCTGCC | H219514 | 1 | 13 | 3 | 4 | 1 | H11641 | ym17e04.s1 Homo sapiens cDNA clone 47962 3' simila |
| | | | | | | | | R95667 | yq51a09.s1 Homo sapiens cDNA clone 199288 3' simil |
| 53 | CATGTCCCGTACAC | H875282 | 1 | 13 | 0 | 0 | 1 | | |
| 54 | CATGATGTAAAAAAT | H241665 | 0 | 11 | 0 | 12 | 14 | M74090 | Human TB2 gene mRNA, 3' end. |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | J03801 | Human lysozyme mRNA, complete cds with an Alu repe |
| | | | | | | | | M19045 | Human lysozyme mRNA, complete cds. |
| 55 | CATGCCAGCCCCCGTC | H337244 | 0 | 11 | 0 | 0 | 0 | | |
| 56 | CATGACCATTCTGCT | H85882 | 0 | 10 | 1 | 26 | 3 | X57351 | Human 1-8D gene from interferon-inducible gene fam |
| | | | | | | | | X02490 | Human interferon-inducible mRNA (cDNA 1-8). |
| 57 | CATGAGGACCATCGC | H165175 | 0 | 10 | 0 | 0 | 0 | | |
| 58 | CATGATGTGAAGAGT(A) | H243747 | 0 | 10 | 0 | 165 | 0 | J03040 | Human SPARC/osteonectin mRNA, complete cds. |
| 59 | CATGCAGTTGGTTGT | H310975 | 0 | 10 | 6 | 7 | 4 | U55217 | Human RNA fragment from patients with Crohn's dise |
| 60 | CATGGCCCTCTGCCA | H613862 | 0 | 10 | 2 | 15 | 7 | | |
| 61 | CATGTTAGATAAGCA | H992010 | 0 | 10 | 3 | 3 | 6 | M94083 | Human chaperonin-like protein (HTR3) mRNA, complet |
| | | | | | | | | L27706 | Human chaperonin protein (Tcp20) gene complete cds |

# Transcripts increased in both colon primary tumors and colon cancer cell lines compared to normal colon (47 genes)

NC: Normal Colon
TU: Colon Primary Tumor
CL: Colon Cancer Cell Line
PT: Pancreatic Primary Tumor
PC: Pancreatic Cancer Cell Line

| # | Tag Sequence | Tag_Number | NC | CT | CL | PT | PC | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGGCAGCCATCCG | H599350 | 87 | 180 | 230 | 72 | 138 | U14969 | Human ribosomal protein L28 mRNA, complete cds. |
| 2 | CATGATGGCTGGTAT | H239533 | 52 | 153 | 318 | 80 | 294 | X17206 | Human mRNA for LLRep3. |
| 3 | CATGCCCGTCCGGAA | H355689 | 87 | 142 | 246 | 178 | 250 | X64707 | H.sapiens BBC1 mRNA |
| 4 | CATGAGGCTACGGAA | H171113 | 44 | 117 | 167 | 86 | 147 | X56932 | H.sapiens mRNA for 23 kD highly basic protein |
| 5 | CATGAGCACCTCCAG | H148949 | 42 | 116 | 197 | 103 | 190 | Z11692 | H.sapiens mRNA for elongation factor 2. |
| 6 | CATGCTGGGTTAATA | H502724 | 29 | 115 | 160 | 75 | 134 | M81757 | H.sapiens S19 ribosomal protein mRNA, complete cds |
| 7 | CATGGGATTTGGCCT | H671654 | 55 | 108 | 222 | 73 | 185 | M17887 | Human acidic ribosomal phosphoprotein P2 mRNA, com |
| 8 | CATGTACCATCAATA | H807748 | 46 | 107 | 98 | 64 | 189 | X53778 | H.sapiens hng mRNA for uracil DNA glycosylase. |
| | | | | | | | | J02642 | Human glyceraldehyde 3-phosphate dehydrogenase mRN |
| 9 | CATGTGGGCAAAGCC | H959498 | 51 | 103 | 156 | 45 | 152 | Z11531 | H.sapiens mRNA for elongation factor-1-gamma. |
| | | | | | | | | M55409 | Human pancreatic tumor-related protein mRNA, 3' en |
| 10 | CATGAATCCTGTGGA | H55227 | 30 | 95 | 102 | 48 | 156 | Z28407 | H.sapiens mRNA for ribosomal protein L8. |
| 11 | CATGGGACCACTGAA | H660601 | 36 | 92 | 114 | 43 | 63 | X73460 | H.sapiens mRNA for ribosomal protein L3. |
| 12 | CATGAGGGCTTCCAA | H174037 | 47 | 91 | 167 | 91 | 155 | M73791 | Human novel gene mRNA, complete cds. |
| | | | | | | | | M64241 | Human Wilm's tumor-related protein (QM) mRNA, comp |
| | | | | | | | | S35960 | laminin receptor homolog (3' region) [human, mRNA |
| 13 | CATGAAGGTGGAGGA | H44683 | 48 | 91 | 182 | 113 | 215 | X80822 | H.sapiens mRNA for ORF. |
| 14 | CATGTGCACGTTTTC | H935680 | 45 | 87 | 105 | 61 | 122 | X03342 | Human mRNA for ribosomal protein L32 |
| 15 | CATGTCAGATCTTTG | H861056 | 37 | 81 | 93 | 50 | 92 | M58458 | Human ribosomal protein S4 (RPS4X) isoform mRNA, c |
| | | | | | | | | M22146 | Human scar protein mRNA, complete cds. |
| 16 | CATGTGGTGTTGAGG | H965603 | 42 | 79 | 83 | 55 | 250 | X69150 | H.sapiens mRNA for ribosomal protein S18. |
| | | | | | | | | L06432 | Homo sapiens 18S ribosomal protein (HKE3) mRNA seq |
| 17 | CATGCCTAGCTGGAT | H379369 | 28 | 77 | 80 | 46 | 143 | Y00052 | Human mRNA for T-cell cyclophilin. |
| 18 | CATGCTTGGGTTTTG | 518912 | 0 | 73 | 42 | 0 | 0 | X07868 | Human DNA for insulin-like growth factor II (IGF-2); |
| 19 | CATGCTCCTCACCTG | H482584 | 12 | 72 | 41 | 34 | 50 | U16811 | Human Bak mRNA, complete cds. |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 20 | CATGCTGTTGGTGAT | H507577 | 17 | 65 | 116 | 48 | 103 | D14530 | Human homolog of yeast ribosomal protein S28, comp |
| 21 | CATGCGCCGGAACAC | H416261 | 28 | 62 | 183 | 55 | 94 | X73974 | H.sapiens HRPL4 mRNA. |
| 22 | CATGCAATAAATGTT | H274492 | 9 | 60 | 73 | 55 | 119 | D23661 | Human mRNA for ribosomal protein L37, complete cds |
| 23 | CATGACATCATCGAT | H79065 | 15 | 57 | 82 | 42 | 118 | L06505 | Human ribosomal protein L12 mRNA, complete cds. |
| 24 | CATGTTCAATAAAAA | H1000193 | 12 | 56 | 154 | 49 | 99 | M17886 | Human acidic ribosomal phosphoprotein P1 mRNA, com |
| 25 | CATGGAACACATCCA | H528694 | 24 | 56 | 71 | 24 | 146 | X63527 | H.sapiens mRNA for ribosomal protein L19. |
| 26 | CATGTTATGGGATCT | H998030 | 7 | 55 | 78 | 35 | 77 | M24194 | Human MHC protein homologous to chicken B complex |
| 27 | CATGGCATAATAGGT | | 18 | 53 | 50 | 19 | 61 | U14967 | Human ribosomal protein L21 mRNA, complete cds. |
| 28 | CATGATTCTCCAGTA | H253260 | 23 | 50 | 103 | 49 | 120 | X55954 | Human mRNA for HL23 ribosomal protein homologue. |
| | | | | | | | | X52839 | Human mRNA for ribosomal protein L17. |
| 29 | CATGACTCCAAAAAA | H119809 | 15 | 49 | 64 | 21 | 64 | H38868 | yp61a04.r1 Homo sapiens cDNA clone 191886 5' simil |
| | | | | | | | | H71935 | ys15f12.r1 Homo sapiens cDNA clone 214895 5'. |
| | | | | | | | | Z43914 | H. sapiens partial cDNA sequence; clone c-1od03. |
| | | | | | | | | T48545 | hbc3221 Homo sapiens cDNA clone hbc3221 5'end. |
| 30 | CATGCTGTTGATTGC | H507455 | 9 | 44 | 54 | 22 | 40 | X04347 | Human liver mRNA fragment DNA binding protein UP1 |
| 31 | CATGTACAAAATCGA | 802871 | 0 | 42 | 20 | 0 | 0 | X00910 | Human mRNA for IGF-II precursor (insulin-like grow |
| 32 | CATGGAAAAATGGTT | H524524 | 14 | 41 | 81 | 15 | 57 | X61156 | H.sapiens mRNA for laminin-binding protein. |
| | | | | | | | | J03799 | Human colin carcinoma laminin-binding protein mRNA |
| 33 | CATGAAGAAGATAGA | H33331 | 9 | 39 | 69 | 30 | 56 | U02032 | Human ribosomal protein L23a mRNA, partial cds. |
| 34 | CATGCCTTCGAGATC | H390692 | 12 | 36 | 51 | 25 | 86 | U14970 | Human ribosomal protein S5 mRNA, complete cds. |
| 35 | CATGACTGGGTCTAT | H125661 | 5 | 29 | 25 | 25 | 38 | X58965 | H.sapiens RNA for nm23-H2 gene. |
| | | | | | | | | M36981 | Human putative NDP kinase (nm23-H2S) mRNA, complet |
| | | | | | | | | L16785 | Homo sapiens c-myc transcription factor (puf) mRNA |
| 36 | CATGCAGCTCACTGA | H302367 | 9 | 29 | 40 | 27 | 31 | L10376 | Human (clone CTG-B33) mRNA sequence. |
| | | | | | | | | S80520 | CAG-isl 7 {trinucleotide repeat-containing sequenc |
| 37 | CATGGTGTGTTTGTA | H769020 | 0 | 24 | 15 | 22 | 8 | M77349 | Human transforming growth factor-beta induced gene |
| 38 | CATGGTGCGCTGAGC | H760291 | 0 | 22 | 17 | 44 | 18 | X58536 | Human mRNA for HLA class I locus C heavy chain. |
| 39 | CATGGTTCACATTAG | H774461 | 3 | 22 | 25 | 141 | 10 | X00497 | Human mRNA for HLA-DR antigens associated invarian |
| 40 | CATGTGAAATAAAAC | H918273 | 2 | 18 | 37 | 8 | 22 | X16934 | Human hB23 gene for B23 nucleophosmin. |
| 41 | CATGAAAAGAAACTT | H2056 | 1 | 16 | 27 | 11 | 25 | Y00345 | Human mRNA for polyA binding protein. |
| 42 | CATGTGCTGCCTGTT | H948604 | 1 | 15 | 16 | 11 | 3 | X81005 | H.sapiens HCG IV mRNA. |
| | | | | | | | | D28137 | Human mRNA for BST-2, complete cds. |
| 43 | CATGCTGATGGCAGA | H495251 | 0 | 14 | 15 | 8 | 6 | W46476 | Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324128 3'. |
| | | | | | | | | X72718 | H.sapiens DNA for orphan TCR V-beta segment (allel |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 44 | CATGACTCGCTCTGT | H121311 | 0 | 12 | 16 | 5 | 7 | H121311 | Soares fetal heart NbHH19W Homo sapiens cDNA clone 342926 3': |
| | | | | | | | | AA305589 | EST176663 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end |
| 45 | CATGGCCCAAGGACC | H610466 | 0 | 12 | 19 | 82 | 17 | X53416 | Human mRNA for actin-binding protein (filamin) (AB |
| 46 | CATGATCTTGTTACT | H229106 | 0 | 11 | 28 | 67 | 0 | X02761 | Human mRNA for fibronectin (FN precursor). |
| 47 | CATGAAGCTGCTGGA | H40571 | 0 | 10 | 17 | 6 | 6 | Z26305 | H.sapiens isoform 1 gene for L-type calcium channe |

# Transcripts increased in only colon cancer cell lines compared to normal colon (181 genes)

NC: Normal Colon
TU: Colon Primary Tumor
CL: Colon Cancer Cell Line
PT: Pancreatic Primary Tumor
PC: Pancreatic Cancer Cell Line

| # | Tag Sequence | Tag_Number | NC | TU | CL | PT | PC | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGTGTGTTGAGAG | H978825 | 71 | 79 | 487 | 136 | 412 | X16869 | Human mRNA for elongation factor 1-alpha |
| 2 | CATGGCCGAGGAAGG | H615043 | 72 | 66 | 265 | 105 | 125 | X53505 | Human ribosomal protein S12. |
| 3 | CATGCAAACCATCCA | H263478 | 137 | 83 | 245 | 36 | 502 | X12883 | Human cytokeratin 18. |
| 4 | CATGCACAAACGGTA | H278636 | 63 | 53 | 201 | 74 | 179 | L19739 | Homo sapiens metallopanstimulin (MPS1) |
| 5 | CATGAAAAAAAAAAA | H1 | 31 | 48 | 186 | 66 | 102 | X83412 | H.sapiens B1 mRNA for mucin. |
| | | | | | | | | Z32564 | H.sapiens FRGAMMA mRNA (819bp) for folate receptor |
| | | | | | | | | X76180 | H.sapiens mRNA for lung amiloride sensitive Na+ ch |
| | | | | | | | | U08470 | Human FR-gamma' mRNA, complete cds. |
| | | | | | | | | U08471 | Human folate receptor 3 mRNA, complete cds. |
| | | | | | | | | S64030 | Human L41 ribosomal protein |
| 6 | CATGTTGGTCCTCTG | H1027448 | 115 | 128 | 179 | 104 | 358 | T91925 | ye02f02.r1 Homo sapiens cDNA clone 116571 5'. |
| 7 | CATGTCTCCATACCC | H906438 | 0 | 0 | 176 | 48 | 0 | X66699 | H.sapiens ribosomal protein L37a. |
| 8 | CATGAAGACAGTGGC | H33979 | 59 | 61 | 172 | 55 | 252 | M60854 | Human ribosomal protein S16 |
| 9 | CATGCCGTCCAAGGG | H374027 | 50 | 39 | 138 | 60 | 108 | M92381 | Human thymosin beta 10 |
| 10 | CATGGGGGAAATCGC | H696375 | 90 | 90 | 136 | 203 | 231 | X69181 | H.sapiens mRNA for ribosomal protein L31. |
| 11 | CATGAAGGAGATGGG | H41531 | 30 | 37 | 133 | 38 | 161 | U14968 | Human ribosomal protein L27a |
| 12 | CATGGAGGGAGTTTC | H567488 | 38 | 53 | 112 | 65 | 142 | X79234 | H.sapiens ribosomal protein L11. |
| 13 | CATGCGCTGGTTCCA | H424694 | 42 | 64 | 111 | 53 | 49 | J03537 | Human ribosomal protein S6 |
| 14 | CATGGCCGTGTCCGC | H618199 | 56 | 39 | 109 | 28 | 120 | U58682 | Human ribosomal protein S28 mRNA, complete cds |
| 15 | CATGGACGACACGAG | H549145 | 32 | 59 | 105 | 44 | 70 | X52839 | Human mRNA for ribosomal protein L17 |
| 16 | CATGTCACCCACACC | H857362 | 36 | 48 | 103 | 44 | 65 | U12465 | Human ribosomal protein L35 |
| 17 | CATGCGCCGCCGGCT | H416106 | 39 | 43 | 90 | 52 | 184 | M17885 | Human acidic ribosomal phosphoprotein P0 |
| 18 | CATGCTCAACATCTC | H475448 | 27 | 41 | 89 | 27 | 145 | M23725 | Human M2-type pyruvate kinase mRNA, complete cds. |
| 19 | CATGTGGCCCCACCC | H955718 | 20 | 30 | 80 | 46 | 55 | M26252 | Human TCB gene encoding cytosolic thyroid hormone- |
| | | | | | | | | M11147 | Human ferritin L chain |
| 20 | CATGCCCTGGGTTCT | H359102 | 34 | 49 | 78 | 92 | 145 | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 21 | CATGAGCATCTCCAG | H150997 | 0 | 0 | 77 | 0 | 0 | H09058 | yl96f11.r1 Homo sapiens cDNA clone 45943 5'. |
| | | | | | | | | Z44640 | H. sapiens partial cDNA sequence; clone c-26b05. |
| | | | | | | | | N75111 | yz29e01.r1 Homo sapiens cDNA clone 284472 5'. |
| 22 | CATGGCCTGTATGAG | H621369 | 24 | 32 | 77 | 33 | 99 | M31520 | Human ribosomal protein S24 mRNA. |
| 23 | CATGAGCTCTCCCTG | H161624 | 33 | 39 | 76 | 21 | 67 | X53777 | Human L23 mRNA for putative ribosomal protein. |
| 24 | CATGCCAGGAGGAAT | H338081 | 27 | 12 | 74 | 23 | 87 | AA223340 | gb\|AA223340\|AA223340 Homo sapiens cDNA clone 650651 3' similar to gb:Y00371_rna1 HEAT SHOCK COGNATE 71 KD PROTEIN (HUMAN) |
| 25 | CATGGGCAAGCCCCA | H672342 | 30 | 55 | 72 | 27 | 61 | U12404 | Human Csa-19 |
| 26 | CATGAGGAAAGCTGC | H163999 | 31 | 42 | 70 | 32 | 146 | F16378 | H.sapiens EST sequence (135-18) from skeletal muscle |
| 27 | CATGAACGCGGCCAA | H26261 | 29 | 46 | 69 | 54 | 79 | Z23063 | Homo sapiens macrophage migration inhibitory factor |
| 28 | CATGCCAGAACAGAC | H335945 | 23 | 39 | 66 | 42 | 148 | X79238 | H.sapiens ribosomal protein L30. |
| 29 | CATGGCCGCCATCTC | H615736 | 7 | 10 | 65 | 10 | 22 | U55017 | Human transketolase (TKT) |
| 30 | CATGGTGTTAACCAG | H769045 | 16 | 19 | 65 | 17 | 76 | L25899 | Human ribosomal protein L10 |
| 31 | CATGCCTCGGAAAAT | H383489 | 9 | 13 | 64 | 23 | 46 | Z26876 | H.sapiens ribosomal protein L38. |
| 32 | CATGAGGTCCTAGCC | H177610 | 15 | 27 | 63 | 43 | 41 | X06547 | Human class Pi glutathione S-transferase |
| 33 | CATGGTTCCCTGGCC | H775658 | 31 | 26 | 63 | 32 | 96 | X65923 | H.sapiens fau mRNA. |
| 34 | CATGTAAGGAGCTGA | H796831 | 32 | 58 | 62 | 42 | 68 | X77770 | H.sapiens RPS26 |
| 35 | CATGAACTAAAAAAA | H28673 | 7 | 14 | 60 | 17 | 39 | W52460 | zc45e11.r1 Soares senescent fibroblasts NbHSF Homo |
| | | | | | | | | N92893 | zb71h03.s1 Homo sapiens cDNA clone 309077 3'. |
| 36 | CATGATTTGTCCCAG | H260949 | 17 | 13 | 57 | 9 | 91 | X14957 | Human hmgl mRNA for high mobility group protein I. |
| 37 | CATGATAATTCTTTG | H200576 | 13 | 27 | 53 | 30 | 69 | U14973 | Human ribosomal protein S29 |
| 38 | CATGCCCCAGCCAGT | H348756 | 18 | 23 | 53 | 5 | 85 | U14990 | Human XP1PO ribosomal protein S3 (rpS3) |
| 39 | CATGGGAGTGGACAT | H667269 | 15 | 13 | 49 | 13 | 45 | L11566 | Homo sapiens ribosomal protein L18 (RPL18) |
| 40 | CATGTAAAAAAAAAA | H786433 | 13 | 8 | 48 | 10 | 26 | H08238 | yl87a01.r1 Homo sapiens cDNA clone 44932 5'. |
| 41 | CATGGTGTTGCACAA | H769605 | 19 | 21 | 48 | 21 | 47 | X79239 | H.sapiens ribosomal protein S13. |
| 42 | CATGGCCAGCCCAGC | H608595 | 6 | 21 | 47 | 11 | 15 | U31657 | Human unknown protein mRNA, partial cds. |
| | | | | | | | | H41030 | yn92a10.r1 Homo sapiens cDNA clone 175866 5'. |
| 43 | CATGGGCTCCCACTG | H685384 | 14 | 24 | 47 | 23 | 15 | M16660 | Human 90-kDa heat-shock protein |
| 44 | CATGTCAACTTCTGG | H853983 | 0 | 0 | 46 | 2 | 0 | N57419 | yw82e04.r1 Homo sapiens cDNA clone 258750 5' simil |
| 45 | CATGGATGCTGCCAA | H583573 | 6 | 12 | 46 | 27 | 18 | X59357 | Human mRNA for Epstein-Barr virus small RNAs (EBER) |
| | | | | | | | | L21756 | Homo sapiens acute myeloid leukemia associated protein |
| | | | | | | | | D17652 | Human mRNA for HBp15/L22, complete cds. |
| 46 | CATGAATAGGTCCAA | H51925 | 13 | 31 | 46 | 47 | 53 | M64716 | Human ribosomal protein S25 |
| 47 | CATGGCTTTTAAGGA | H655115 | 8 | 26 | 45 | 22 | 63 | L06498 | Homo sapiens ribosomal protein S20 (RPS20) |
| 48 | CATGAATGCAGGCAG | H58533 | 2 | 12 | 44 | 6 | 27 | M61831 | Human S-adenosylhomocysteine hydrolase (AHCY) |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 49 | CATGGCCCAGCTGGA | H610939 | 8 | 18 | 43 | 0 | 22 | Z21507 | Human elongation factor 1 delta (EF 1delta) |
| 50 | CATGGGCCGCGTTCG | H678334 | 6 | 6 | 42 | 8 | 18 | M13932 | Human ribosomal protein S17 mRNA |
| 51 | CATGTGAGGGAATAA | H928269 | 14 | 26 | 42 | 15 | 42 | M10036 | Human triosephosphate isomerase |
| 52 | CATGTGTACCTGTAA | H968173 | 14 | 24 | 42 | 35 | 49 | K00558 | human alpha-tubulin |
| 53 | CATGGGCAAGAAGAA | H672265 | 8 | 7 | 41 | 12 | 87 | L19527 | Homo sapiens ribosomal protein L27 (RPL27) |
| 54 | CATGAACTAACAAAA | H28737 | 6 | 14 | 40 | 14 | 15 | X63237 | H.sapiens Uba80 mRNA for ubiquitin. |
| 55 | CATGTATACGCTCAG | H837237 | 0 | 0 | 38 | 0 | 9 | | Unknown |
| 56 | CATGTACAAGAGGAA | H803369 | 7 | 17 | 38 | 14 | 42 | X69391 | H.sapiens ribosomal protein L6. |
| 57 | CATGGTTAACGTCCC | H770486 | 8 | 17 | 38 | 12 | 25 | H11182 | ym14a02.r1 Homo sapiens cDNA clone 47866 5' |
| | | | | | | | | T40302 | ya31g04.r5 Homo sapiens cDNA clone 62262 5' |
| | | | | | | | | T89480 | yd98a05.r1 Homo sapiens cDNA clone 116240 5' |
| 58 | CATGGAGACTCCTGC | H558943 | 13 | 12 | 38 | 32 | 10 | H01362 | yi99c06.r1 Homo sapiens cDNA clone 147370 5' |
| 59 | CATGATCCACATCGC | H217399 | 3 | 10 | 37 | 10 | 14 | H94371 | yw54e05.r1 Homo sapiens cDNA clone 256064 5'. |
| | | | | | | | | T49412 | ya75b09.r1 Homo sapiens cDNA clone 67481 5'. |
| | | | | | | | | T51058 | yb55a12.r1 Homo sapiens cDNA clone 75070 5'. |
| 60 | CATGGAAGCTTTGCA | H534522 | 11 | 13 | 37 | 14 | 25 | X07270 | Human heat shock protein hsp86. |
| 61 | CATGCTGGCGAGCGC | H501287 | 2 | 9 | 36 | 3 | 18 | M91670 | Human ubiquitin carrier protein (E2-EPF) |
| 62 | CATGCTGAGACAAAG | H493633 | 13 | 8 | 36 | 8 | 26 | X74070 | H.sapiens transcription factor BTF 3. |
| 63 | CATGAACGACCTCGT | H24951 | 7 | 13 | 35 | 22 | 40 | V00599 | Human beta-tubulin |
| 64 | CATGGCATAGGCTGC | H602783 | 9 | 16 | 35 | 2 | 17 | X84694 | H.sapiens mRNA for elongations factor Tu-mitochondria |
| | | | | | | | | L38995 | Homo sapiens nuclear-encoded mitochondrial elongatation factor |
| | | | | | | | | S75463 | P43=mitochondrial elongation factor homolog [human |
| 65 | CATGCATCTTCACCA | H319302 | 12 | 14 | 35 | 9 | 16 | H48893 | yq80b12.r1 Homo sapiens cDNA clone 202079 5' |
| 66 | CATGGCCTGCTGGGC | H621035 | 10 | 5 | 32 | 18 | 107 | X71973 | H.sapiens GPx-4 mRNA for phospholipid hydroperoxidase |
| 67 | CATGACAGGCTACGG | H76231 | 0 | 5 | 31 | 64 | 0 | M95787 | Human 22kDa smooth muscle protein (SM22) |
| 68 | CATGGAAATGTAAGA | H528067 | 5 | 12 | 31 | 14 | 25 | H80294 | yu59g01.s1 Homo sapiens cDNA clone 230448 3'. |
| | | | | | | | | R74294 | yi57f06.r1 Homo sapiens cDNA clone 143363 5'. |
| 69 | CATGGAAGCCAGCCA | H533798 | 1 | 3 | 30 | 9 | 11 | L36055 | Human 4E-binding protein 1 |
| 70 | CATGTTACCATATCA | H988366 | 10 | 28 | 30 | 19 | 86 | F17005 | H.sapiens EST sequence (011-T1-18) from skeletal muscle |
| 71 | CATGTTGCTCACAAA | H1023249 | 1 | 2 | 29 | 1 | 2 | H10519 | yl90g04.r1 Homo sapiens cDNA clone 45563 5'. |
| 72 | CATGTCCCCGCTCGA | H874103 | 0 | 6 | 29 | 0 | 0 | | Unknown |
| 73 | CATGATTAACAAAGC | H246019 | 8 | 9 | 29 | 25 | 26 | X04409 | Human coupling protein G(s) alpha-subunit |
| 74 | CATGCAGATCTTTGT | H298495 | 2 | 7 | 28 | 8 | 24 | X56998 | Human UbA52 adrenal mRNA for ubiquitin-52 amino acid |
| 75 | CATGGTTCGTGCCAA | H777109 | 9 | 28 | 28 | 17 | 46 | F19234 | H.sapiens EST sequence (005-X3-16) from skeletal m |
| 76 | CATGGACGTGTGGGC | H552683 | 3 | 4 | 27 | 2 | 16 | X52317 | Human histone H2A.Z. |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 77 | CATGCTAAAAAAAAA | H458753 | 4 | 8 | 27 | 19 | 8 | M33680 | Human 26-kDa cell surface protein TAPA-1 |
| 78 | CATGGGGTTTTTATT | H704500 | 4 | 1 | 27 | 6 | 18 | L28809 | Homo sapiens dbpB-like protein |
| 79 | CATGCCGATCACCGG | H363799 | 7 | 9 | 27 | 7 | 15 | M29536 | Human translational initiation factor 2 beta subunit |
| 80 | CATGGCACAAGAAGA | H594051 | 6 | 9 | 26 | 7 | 29 | W07137 | za92a11.r1 Soares fetal lung NbHL19W Homo sapiens |
| | | | | | | | | D20503 | Human HL60 3'directed MboI cDNA, HUMGS01477, clone |
| | | | | | | | | N91592 | Soares fetal lung NbHL19W Homo sapiens cDNA clone 303055 3'. |
| | | | | | | | | H83884 | yv84c07.s1 Homo sapiens cDNA clone 249420 3' similar to contains Alu repetitive element;. |
| 81 | CATGTCTCTACCCAC | H908373 | 7 | 11 | 26 | 11 | 13 | Z22572 | H.sapiens CDEI binding protein mRNA. |
| | | | | | | | | L09209 | Homo sapiens amyloid protein homologue mRNA, compl |
| | | | | | | | | L19597 | Human binding protein mRNA, partial cds. |
| | | | | | | | | S60099 | APPH=amyloid precursor protein homolog [human, pla |
| 82 | CATGGTTTCCCCAAG | H783697 | 1 | 0 | 25 | 3 | 0 | W07587 | zb06f02.r1 Soares fetal lung NbHL19W Homo sapiens |
| | | | | | | | | N28502 | yx36f06.r1 Homo sapiens cDNA clone 263843 5' |
| | | | | | | | | N35630 | yx62a03.r1 Homo sapiens cDNA clone 266284 5' |
| 83 | CATGCCTGTCCAGCC | H388426 | 2 | 3 | 25 | 3 | 13 | Z40265 | H. sapiens partial cDNA sequence; clone c-1xe03. |
| | | | | | | | | W02723 | zc65c03.s1 Soares fetal heart NbHH19W Homo sapiens |
| | | | | | | | | N24893 | yx99h09.s1 Homo sapiens cDNA clone 269921 3'. |
| | | | | | | | | N32178 | yy25b09.s1 Homo sapiens cDNA clone 272249 3'. |
| 84 | CATGTCATCATCTGA | H865503 | 5 | 15 | 25 | 5 | 7 | H21873 | yl34b10.s1 Homo sapiens cDNA clone 160123 3' simil |
| | | | | | | | | H26394 | yl48e12.s1 Homo sapiens cDNA clone 161518 3' simil |
| | | | | | | | | H69857 | yr88d02.s1 Homo sapiens cDNA clone 212355 3' simil |
| | | | | | | | | H70714 | yu69b11.s1 Homo sapiens cDNA clone 239037 3' simil |
| 85 | CATGCCCTGCCTTGT | H358783 | 5 | 8 | 25 | 16 | 31 | X55110 | Human mRNA for neurite outgrowth-promoting protein |
| 86 | CATGGCCGGGCCCTC | H617048 | 1 | 1 | 24 | 0 | 1 | X03168 | Human mRNA for S-protein. |
| 87 | CATGTTGCTCAAAAA | H1023233 | 2 | 1 | 24 | 2 | 2 | AA143561 | zo32d09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588593 3' similar to contains LTR7.t1 LTR7 repetitive element |
| | | | | | | | | AA152342 | zo01g11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 566468 3' similar to contains LTR7.t3 LTR7 repetitive element ; |
| | | | | | | | | AA115727 | zl86h11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511557 3' similar to contains LTR7.t1 LTR7 repetitive element |
| 88 | CATGCAAAATCAGGA | H262987 | 6 | 2 | 24 | 5 | 15 | R76502 | yi61f09.r1 Homo sapiens cDNA clone 143753 5'. |
| | | | | | | | | T32681 | EST52915 Homo sapiens cDNA 5' end similar to None. |
| | | | | | | | | T34662 | EST72468 Homo sapiens cDNA 5' end similar to None. |
| 89 | CATGGAAGATGTGGG | H533435 | 1 | 5 | 23 | 4 | 7 | H04634 | yj49h03.r1 Homo sapiens cDNA clone 152117 5'. |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | F00364 | H. sapiens partial cDNA sequence; clone 76D12; ver |
| 90 | CATGGTGCTCATTCA | H761150 | 0 | 8 | 23 | 6 | 4 | H01503 | yj21c05.s1 Homo sapiens cDNA clone 149384 3'. |
| | | | | | | | | H84813 | yv86c02.s1 Homo sapiens cDNA clone 249602 3' simil |
| | | | | | | | | H84956 | yv88f07.s1 Homo sapiens cDNA clone 249829 3' simil |
| 91 | CATGGCTTTACTTTG | H654464 | 4 | 5 | 23 | 9 | 5 | L38961 | Homo sapiens putative transmembrane protein (B5) |
| 92 | CATGTTTTCTGAAAA | H1046401 | 6 | 13 | 23 | 10 | 10 | J04026 | Human thioredoxin (TXN) mRNA |
| 93 | CATGTTGCTCACACA | H1023250 | 1 | 4 | 22 | 0 | 4 | D11078 | Human RGH2 gene. |
| 94 | CATGGATTTCTCAGC | H589267 | 0 | 0 | 22 | 0 | 19 | X53279 | Human mRNA for placental-like alkaline phosphatase |
| 95 | CATGAGGAGGGAGGC | H166539 | 2 | 3 | 22 | 2 | 4 | M77836 | Human pyrroline 5-carboxylate reductase mRNA, |
| 96 | CATGGCTTAACCTGG | H651359 | 3 | 4 | 22 | 2 | 4 | X07674 | Human glutamate dehydrogenase |
| 97 | CATGCTCTTCGAGAA | H490889 | 4 | 8 | 22 | 27 | 19 | Y00433 | Human mRNA for glutathione peroxidase |
| 98 | CATGAGAACAAAACC | H132098 | 1 | 7 | 21 | 9 | 6 | X67951 | H.sapiens mRNA for proliferation-associated gene |
| 99 | CATGCCCAGGGAGAA | H346761 | 3 | 3 | 21 | 2 | 24 | U38846 | Human stimulator of TAR RNA binding (SRB) |
| | | | | | | | | D16933 | Human HepG2 3' region cDNA, clone hmd4f11. |
| 100 | CATGCACTTCAAGGG | H294155 | 0 | 3 | 20 | 47 | 107 | U42376 | Human retinoic acid induced RIG-E |
| 101 | CATGGCGGAGAGAGG | H631331 | 2 | 3 | 20 | 4 | 1 | | Unknown |
| 102 | CATGTTACCTCCTTC | H1989024 | 4 | 7 | 20 | 3 | 22 | F17524 | H.sapiens EST sequence (012-T2-32) from skeletal m |
| 103 | CATGACTCTGCCAAG | H122449 | 4 | 7 | 20 | 3 | 7 | | Unknown |
| 104 | CATGTCAGATGGCGT | H861095 | 1 | 6 | 19 | 12 | 7 | W52942 | zc03h05.r1 Soares parathyroid tumor NbHPA Homo sap |
| 105 | CATGGGCCTTTTTTT | H679936 | 1 | 3 | 19 | 5 | 3 | R21316 | yg48h11.r1 Homo sapiens cDNA clone 35917 5' simila |
| 106 | CATGTGGACGCGCTG | H951912 | 0 | 0 | 19 | 0 | 0 | X00566 | Human lipoprotein apoA1. |
| 107 | CATGCCTGCTCCCTG | H386904 | 0 | 5 | 19 | 6 | 5 | M80244 | Human E16 mRNA |
| 108 | CATGGCCACACCCCA(C) | H607318 | 2 | 6 | 18 | 18 | 15 | H27927 | yl58c11.s1 Homo sapiens cDNA clone 162452 3' simil |
| 109 | CATGATTATTTTTCT | H249854 | 2 | 3 | 18 | 5 | 20 | X57959 | H.sapiens ribosomal protein L7. |
| 110 | CATGGAACCCTGGGA | H529899 | 2 | 7 | 18 | 5 | 15 | AA299898 | EST12509 Uterus tumor I Homo sapiens cDNA 5' end |
| 111 | CATGGGCTGATGTGG | H686319 | 3 | 5 | 18 | 8 | 17 | U09510 | Human glycyl-tRNA synthetase . |
| 112 | CATGTCAATAAAGAA | H855049 | 3 | 10 | 18 | 4 | 4 | X76013 | H.sapiens QRSHs mRNA for glutaminyl-tRNA synthetas |
| 113 | CATGAAAGTGAAGAT | H11785 | 0 | 7 | 17 | 0 | 5 | W16529 | zb10a11.r1 Soares fetal lung NbHL19W Homo sapiens |
| | | | | | | | | W35192 | zc70b05.r1 Soares fetal heart NbHH19W Homo sapiens |
| | | | | | | | | W52451 | zc45d09.r1 Soares senescent fibroblasts NbHSF Homo |
| 114 | CATGCACGCGCTCAA | H288373 | 0 | 1 | 17 | 0 | 3 | D38251 | Human mRNA for RPB5 (XAP4) |
| 115 | CATGAACTAATACTA | H28872 | 1 | 6 | 17 | 13 | 31 | D52570 | Human fetal brain cDNA 5'-end GEN-081G12. |
| | | | | | | | | D52758 | Human fetal brain cDNA 5'-end GEN-087A08. |
| | | | | | | | | D55953 | Human fetal brain cDNA 5'-end GEN-407H12. |
| 116 | CATGCTGTACCTGGA | H504187 | 1 | 0 | 17 | 12 | 6 | M22490 | Human bone morphogenetic protein-2B (BMP-2B) |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 117 | CATGCGACCCCACGC | H398663 | 2 | 6 | 17 | 48 | 0 | M12529 | Human apolipoprotein E |
| 118 | CATGTAGAAAAATAA | H819213 | 0 | 1 | 16 | 2 | 7 | X16539 | H.sapiens RNA for neuroleukin gene. |
| | | | | | | | | M27691 | Human transactivator protein (CREB) mRNA, complete |
| 119 | CATGATCTTGAAAGG | H228867 | 0 | 0 | 16 | 5 | 3 | M86667 | H.sapiens NAP (nucleosome assembly protein) |
| 120 | CATGCAGCTGGCCAT | H302741 | 0 | 1 | 16 | 14 | 0 | X53743 | H.sapiens mRNA for fibulin-1 C. |
| 121 | CATGATCTTGAAAGG | H228867 | 0 | 0 | 16 | 5 | 3 | Z26328 | H. sapiens partial cDNA sequence; clone HEC059 |
| 121 | CATGATCTTGAAAGG | H228867 | 0 | 0 | 16 | 5 | 3 | Z26328 | H. sapiens partial cDNA sequence; clone HEC059 |
| 122 | CATGGTGGAGGTGCG | H762554 | 2 | 10 | 16 | 3 | 5 | U22055 | Human 100 kDa coactivator mRNA |
| 123 | CATGGTGGACCCCAA | H762197 | 1 | 5 | 15 | 7 | 10 | R91724 | yp98e02.r1 Homo sapiens cDNA clone 195482 5' simil |
| | | | | | | | | W51770 | zc48a02.r1 Soares senescent fibroblasts NbHSF Homo |
| | | | | | | | | N42086 | yy05b03.r1 Homo sapiens cDNA clone 270317 5' |
| 124 | CATGGAGCAGCTGGA | H561787 | 0 | 5 | 15 | 2 | 4 | R80990 | yi94c02.r1 Homo sapiens cDNA clone 146882 5' |
| | | | | | | | | R95056 | yq44f01.r1 Homo sapiens cDNA clone 198649 5' simil |
| 125 | CATGGCGGGAGGGCT | H633002 | 1 | 6 | 15 | 8 | 7 | F16507 | H.sapiens EST sequence (147-09) from skeletal musc |
| | | | | | | | | T50201 | yb77h05.r1 Homo sapiens cDNA clone 77241 5' simila |
| 126 | CATGATTGGCTTAAA | H256497 | 1 | 8 | 15 | 0 | 16 | S85655 | Human prohibitin |
| 127 | CATGGAAAAATTTAA | H524541 | 0 | 3 | 15 | 4 | 0 | M38188 | Human unknown protein from clone pHGR74 mRNA, comp |
| 128 | CATGGATCACAGTTT | H577840 | 0 | 5 | 15 | 0 | 0 | Y00711 | Human lactate dehydrogenase B (LDH-B). |
| 129 | CATGAGCCTTTGTTG | H155632 | 1 | 2 | 15 | 23 | 5 | D83174 | Human collagen binding protein 2. |
| 130 | CATGTCTGCACCTCC | H910430 | 0 | 0 | 15 | 0 | 2 | X70940 | H.sapiens elongation factor 1 alpha-2. |
| 131 | CATGAACAGAAGCAA | H18469 | 0 | 2 | 15 | 3 | 11 | T30623 | EST19638 Homo sapiens cDNA 5' end similar to None. |
| | | | | | | | | C01011 | HUMGS0004747, Human Gene Signature, 3'-directed cDNA sequence. |
| | | | | | | | | AA111865 | zm62d06.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone 530219 3' |
| | | | | | | | | W56516 | zd16c08.r1 Soares fetal heart NbHH19W Homo sapiens |
| 132 | CATGTGTTCAGGACC | H980130 | 1 | 1 | 14 | 5 | 11 | H30299 | yo77d04.r1 Homo sapiens cDNA clone 183943 5' simil |
| | | | | | | | | H50265 | yo28c02.r1 Homo sapiens cDNA clone 179234 5'. |
| 133 | CATGTAGATAATGGC | H822331 | 1 | 4 | 14 | 6 | 14 | W01702 | za37a06.r1 Soares fetal liver spleen 1NFLS Homo sa |
| | | | | | | | | W04495 | za58b10.r1 Soares fetal liver spleen 1NFLS Homo sa |
| | | | | | | | | W23528 | zc71g11.s1 Soares fetal heart NbHH19W Homo sapiens |
| 134 | CATGCTTAATCCTGA | H508767 | 0 | 6 | 14 | 6 | 12 | D11838 | Human HepG2 3'-directed MboI cDNA, clone hm02e09. |
| 135 | CATGGGCAGAGGACC | H673954 | 0 | 6 | 14 | 5 | 11 | X75598 | H.sapiens nm23H1 gene. |
| 136 | CATGTGACTGAAGCC | H925194 | 0 | 5 | 14 | 3 | 0 | T35470 | EST85850 Homo sapiens cDNA 5' end similar to None. |
| | | | | | | | | T35536 | EST86951 Homo sapiens cDNA 5' end similar to None. |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | T35545 | EST87066 Homo sapiens cDNA 5' end similar to None. |
| 137 | CATGGATAGTTGTGG | H576495 | 0 | 1 | 14 | 2 | 1 | H01694 | yj33g11.s1 Homo sapiens cDNA clone 150596 3'. |
| | | | | | | | | N78851 | zb17d08.s1 Homo sapiens cDNA clone 302319 3'. |
| | | | | | | | | N78931 | za92h06.s1 Homo sapiens cDNA clone 300059 3'. |
| 138 | CATGGTGGTGGACAC | H765573 | 1 | 4 | 13 | 6 | 13 | H90469 | yv01e06.r1 Homo sapiens cDNA clone 241474 5' simil |
| | | | | | | | | R76765 | yi63g01.r1 Homo sapiens cDNA clone 143952 5' simil |
| | | | | | | | | T35045 | EST79335 Homo sapiens cDNA similar to None.. |
| 139 | CATGTGGGGTACCTT | H961304 | 0 | 6 | 13 | 2 | 9 | H51447 | yo31a05.r1 Homo sapiens cDNA clone 179504 5'. |
| | | | | | | | | W46469 | zc32c05.r1 Soares senescent fibroblasts NbHSF Homo |
| | | | | | | | | W51800 | zc48e04.r1 Soares senescent fibroblasts NbHSF Homo |
| | | | | | | | | R33196 | yh77f08.r1 Homo sapiens cDNA clone 135783 5'. |
| 140 | CATGTTCATTATAAT | H1003313 | 1 | 10 | 13 | 8 | 10 | J04799 | Human prothymosin-alpha |
| 141 | CATGCTTCTGTGTAC(T) | H515821 | 0 | 5 | 13 | 8 | 12 | D80012 | Human KIAA0190 protein |
| 142 | CATGACTGGCGAAGT | H125315 | 1 | 5 | 13 | 2 | 5 | U02389 | Human hLON ATP-dependent protease mRNA |
| | | | | | | | | T29819 | EST96617 Homo sapiens cDNA 5' end similar to ATP-d |
| 143 | CATGGAAAGAGCTGA | H526495 | 1 | 3 | 13 | 1 | 6 | X14850 | Human histone H2A.X. |
| 144 | CATGCAACTCTATGG | H269775 | 0 | 1 | 13 | 1 | 2 | J04088 | Human DNA topoisomerase II (top2) mRNA |
| 145 | CATGAAATTTGGTGC | H16303 | 0 | 0 | 13 | 0 | 0 | K01891 | Human beta globin retrovirus-like repetitive element |
| | | | | | | | | H88396 | EST28e05 Homo sapiens cDNA clone 28e05 |
| 146 | CATGCTGCACTTACT | H496114 | 1 | 2 | 13 | 1 | 8 | X74796 | H.sapiens p85Mcm mRNA. |
| | | | | | | | | D28480 | Human mRNA for hMCM2, complete cds. |
| | | | | | | | | D55716 | Human B lymphoma mRNA for P1cdc47, complete cds. |
| 147 | CATGAATATTGAGAA | H53129 | 0 | 5 | 13 | 6 | 11 | T30327 | EST14849 Homo sapiens cDNA 5' end similar to None. |
| | | | | | | | | T34394 | EST66942 Homo sapiens cDNA 5' end similar to None. |
| | | | | | | | | T47475 | yb14c03.r1 Homo sapiens cDNA clone 71140 5'. |
| | | | | | | | | T50289 | yb14h08.r1 Homo sapiens cDNA clone 71199 5'. |
| 148 | CATGTCGCCGGGCGC | H890535 | 0 | 1 | 13 | 2 | 1 | | Unknown |
| 149 | CATGGGGGCAGCCG | H697495 | 0 | 2 | 13 | 2 | 7 | H59914 | Unknown |
| 150 | CATGCCAAGAAAGAA | H329737 | 0 | 6 | 12 | 4 | 4 | U33818 | Human inducible poly(A)-binding protein |
| 151 | CATGTTTTTGATAAA | H1048113 | 0 | 5 | 12 | 4 | 12 | D16891 | Human HepG2 3' region cDNA, clone hmd2c11. |
| 152 | CATGTGTGGAGAGCC | H977034 | 0 | 0 | 12 | 0 | 0 | M29882 | Human apolipoprotein A-II |
| 153 | CATGCCCACGGTTAG | H345789 | 0 | 5 | 12 | 5 | 4 | Z49216 | H.sapiens mitoxantrone-resistance associated mRNA. |
| 154 | CATGAATTCTCCTAA | H63325 | 0 | 1 | 12 | 1 | 1 | | Unknown |
| 155 | CATGGACCTCCGGGC | H548203 | 0 | 0 | 12 | 0 | 0 | | Unknown |
| 156 | CATGTGAATCTGGGT | H921067 | 0 | 2 | 11 | 7 | 8 | M93651 | Human set gene |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 157 | CATGTCCTTCTCCAC | H884181 | 0 | 5 | 11 | 14 | 8 | X15804 | Human alpha-actinin. |
| 158 | CATGTATCTGTCTAC | H843485 | 0 | 4 | 11 | 2 | 3 | T19569 | 609F Homo sapiens cDNA clone 609 similar to SET protein |
| 159 | CATGACGTTCTCTTC | H114144 | 0 | 0 | 11 | 1 | 17 | Z36249 | HHEA18W H. sapiens partial cDNA sequence; clone HEA18W; |
| 160 | CATGCCCTGAGTCAG | H358581 | 0 | 0 | 11 | 0 | 0 | AA207189 | zq73e07.r1 Stratagene neuroepithelium (#937231)Homo sapiens cDNA clone 647268 5' similar to TR:E16910 E16910 ENDONUCLEASE. ; |
| 161 | CATGGAATTCCTCGA | H540023 | 0 | 3 | 11 | 3 | 1 | N80776 | za98h04.s1 Homo sapiens cDNA clone 300631 3'. |
| | | | | | | | | AA025809 | ze90d01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366241 3' |
| | | | | | | | | AA279492 | zs85h05.s1 Soares NbHTGBC Homo sapiens cDNA clone 704313 3' |
| 162 | CATGGACGCCGAACT | H550274 | 0 | 1 | 11 | 6 | 0 | | Unknown |
| 163 | CATGGCGGACTGGGG | H631275 | 0 | 0 | 11 | 1 | 0 | AA098867 | zk84f04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489535 3' similar to SW:A5_XENLA P28824 A5 PROTEIN PRECURSOR |
| 164 | CATGGGAACACACAG | H656453 | 0 | 1 | 11 | 0 | 2 | R48460 | yj67c12.r1 Homo sapiens cDNA clone 153814 5'. |
| | | | | | | | | AA173819 | zp01c02.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595106 5' |
| 165 | CATGTTGCGGAGCCC | H1022502 | 0 | 2 | 11 | 2 | 1 | L19183 | HUMMAC30X Human MAC30 mRNA, 3' end. |
| | | | | | | | | H61710 | yr24a07.s1 Homo sapiens cDNA clone 206196 3'. |
| | | | | | | | | H77330 | yu11f12.s1 Homo sapiens cDNA clone 233519 3'. |
| | | | | | | | | N69482 | za18d05.s1 Homo sapiens cDNA clone 292905 3'. |
| 166 | CATGGCAGACATTGA | H598335 | 0 | 7 | 10 | 4 | 9 | H41078 | yp52c11.s1 Homo sapiens cDNA clone 191060 3' simil |
| 167 | CATGCACTTGAAAA | H294401 | 0 | 1 | 10 | 5 | 0 | H04630 | yj49g03.r1 Homo sapiens cDNA clone 152116 5'. |
| 168 | CATGGGTTGGCAGG | H719435 | 0 | 0 | 10 | 24 | 0 | R77027 | yi66e12.r1 Homo sapiens cDNA clone 144238 5'. |
| 169 | CATGTTCCTCGGGC | H1007018 | 0 | 1 | 10 | 4 | 12 | R32331 | yh68g02.s1 Homo sapiens cDNA clone 134930 3' simil |
| 170 | CATGCTGCCGAGCT | -497192 | 0 | 8 | 10 | 1 | 10 | T86566 | yd77g07.r1 Homo sapiens cDNA clone 114300 5' simil |
| 171 | CATGGTGAAAAAAA | H753665 | 0 | 2 | 10 | 3 | 7 | S77357 | transcript ch111 [human, RF1,RF48 stomach cancer c |
| 172 | CATGCTGTGCAGCA | H506149 | 0 | 6 | 10 | 6 | 1 | M34338 | Human spermidine synthase |
| 173 | CATGTAGTTTGTGG | -835515 | 0 | 1 | 10 | 0 | 2 | U03911 | Human mutator gene (hMSH2) |
| 174 | CATGATGTAGTAGTG | H242380 | 0 | 5 | 10 | 9 | 7 | D55671 | Human heterogeneous nuclear ribonucleoprotein |
| 175 | CATGGACCCACTACC | H545906 | 0 | 1 | 10 | 3 | 1 | J03569 | Human lymphocyte activation antigen 4F2 large subunit |
| 176 | CATGAAATAGGTTTT | H12992 | 0 | 1 | 10 | 6 | 3 | D53402 | Human fetal brain cDNA 5'-end GEN-108D03. |
| | | | | | | | | T61971 | yb96f02.r1 Homo sapiens cDNA clone 79035 5'. |
| | | | | | | | | D61243 | Human fetal brain cDNA 5'-end GEN-171G06. |
| | | | | | | | | N77240 | yv44d02.r1 Homo sapiens cDNA clone 245571 5'. |
| 177 | CATGCCGGGCGTGGT | H371131 | 0 | 0 | 10 | 1 | 2 | T35761 | EST90898 Homo sapiens cDNA 5' end similar to EST c |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 178 | CATGGACTGAGCTTG | H555168 | 0 | 8 | 10 | 3 | 3 | T31901 | EST40719 Homo sapiens cDNA 5' end similar to None. |
| 179 | CATGAAACGCCCAAT | H6481 | 0 | 2 | 10 | 1 | 3 | X98264 | IHSMPP41 H.sapiens mRNA for M-phase phosphoprotein, mpp4, 1523bp |
| 180 | CATGATGAGGCCGGG | H232027 | 0 | 4 | 10 | 7 | 1 | | Unknown |
| 181 | CATGGCCCACATCCG(A) | H610614 | 0 | 9 | 10 | 6 | 2 | D87433 | Human mRNA for KIAA0246 gene, partial cds |

Table 3 - Transcripts decreased in colon cancer

# Transcripts decreased in only colon primary tumors compared to normal colon (51 genes)

NC Normal Colon
CT Colon Primary Tumor
CL Colon Cancer Cell Line
PT Pancreatic Primary Tumor
PC Pancreatic Cancer Cell Line

| # | Tag sequence | Tag_Number | NC | CT | CL | PT | PC | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGGCTTTATTTGT | H654591 | 184 | 110 | 185 | 203 | 111 | X00351 | Human mRNA for beta-actin. |
| 2 | CATGCTAGCCTCACG | H468434 | 170 | 61 | 130 | 80 | 75 | X04098 | Human mRNA for cytoskeletal gamma-actin. |
| 3 | CATGCAAACCATCCA | H263478 | 137 | 83 | 245 | 36 | 502 | X12883 | Human mRNA for cytokeratin 18. |
| 4 | CATGCTTCCAGCTAA | H513181 | 64 | 23 | 36 | 53 | 104 | D00017 | Human lipocortin II mRNA. |
| 5 | CATGCCCCAGTTGCT | H348922 | 61 | 27 | 38 | 37 | 46 | X04106 | Human mRNA for calcium dependent protease (small subunit) |
| 6 | CATGGATGACCCCCC | H581974 | 53 | 4 | 42 | 6 | 32 | Z65513 | H.sapiens CpG island DNA genomic Mse1 fragment, cl |
| 7 | CATGCTGTACAGACA | H504098 | 50 | 22 | 26 | 6 | 32 | W61077 | zd30d02.r1 Soares fetal heart NbHH19W Homo sapiens |
| 8 | CATGCGGACTCACTG | H427848 | 47 | 15 | 26 | 18 | 4 | D60944 | Human fetal brain cDNA 5'-end GEN-141D02. |
| 9 | CATGCCCCCGCGGAA | H349801 | 47 | 10 | 21 | 15 | 8 | | Unknown |
| 10 | CATGCCTGGAAGAGG | H387107 | 46 | 19 | 39 | 47 | 14 | J02783 | Human thyroid hormone binding protein (p55) mRNA, |
| 11 | CATGGCCTGGCCATC | H621140 | 46 | 19 | 24 | 16 | 20 | N33042 | yy05d05.s1 Homo sapiens cDNA clone 270345 3' |
| 12 | CATGAGCAGGAGCAG | H150053 | 43 | 12 | 26 | 24 | 20 | W07627 | zb06a05.r1 Soares fetal lung NbHL19W Homo sapiens |
| 13 | CATGAACGTGCAGGG | H28235 | 42 | 6 | 57 | 2 | 10 | X01630 | Human mRNA for argininosuccinate synthetase. |
| 14 | CATGGCCGCCCTGCA | H615802 | 40 | 12 | 16 | 17 | 8 | D43682 | Human mRNA for very-long-chain acyl-CoA dehydrogen |
| 15 | CATGTGGGGAGAGGA | H960651 | 40 | 5 | 36 | 10 | 5 | D29146 | Human keratinocyte cDNA, clone 173. |
| 16 | CATGGCTGCCCTTGA | H648575 | 38 | 10 | 20 | 6 | 39 | K00557 | human alpha-tubulin mRNA, 3' end. |
| 17 | CATGTGGCCATCTGC | H955615 | 37 | 5 | 15 | 19 | 18 | AA341633 | AA341633 EST47188 Fetal kidney II Homo sapiens cDNA 5' end |
| 18 | CATGCGTTCCTGCGG | H456167 | 35 | 4 | 36 | 8 | 0 | X77956 | H.sapiens Id1 mRNA. |
| 19 | CATGTGCATCTGGTG | H937452 | 33 | 9 | 14 | 13 | 10 | X87949 | H.sapiens mRNA for BiP protein. |
| 20 | CATGGTGACCTCCTT | H755160 | 33 | 7 | 12 | 6 | 31 | J04823 | Human cytochrome c oxidase subunit VIII (COX8) mRNa |
| 21 | CATGTAGCTCTATGG | H826831 | 33 | 5 | 18 | 9 | 13 | U16798 | Human Na,K-ATPase alpha-1 subunit mRNA, complete c |
| 22 | CATGGTGCGCTAGGG | H760267 | 29 | 7 | 26 | 19 | 27 | R50350 | gb\|R50350\|R50350 yj59c04.s1 Homo sapiens cDNA clone 153030 3'. |
| | | | | | | | | R50013 | yj59c04.r1 Homo sapiens cDNA clone 153030 5'. |
| | | | | | | | | C02981 | Human Heart cDNA, clone 3NHC0642. |

| | | H694767 | 28 | 6 | 20 | 6 | 26 | T31329 | EST10445 Homo sapiens cDNA 5' end similar to ubiquinol cytochrome-c reductase, 6.4 kDa. |
|---|---|---|---|---|---|---|---|---|---|
| 23 | CATGGGGCGCTGTGG | H382130 | 27 | 6 | 12 | 3 | 19 | | Unknown |
| 24 | CATGCCTCCAGTAC | H388627 | 27 | 3 | 14 | 8 | 7 | H63643 | yr34d11.r1 Homo sapiens cDNA clone 207189 5' simil |
| 25 | CATGCCTGTGACAGC | H856806 | 24 | 5 | 8 | 17 | 11 | W60924 | zd27c08.r1 Soares fetal heart NbHH19W Homo sapiens |
| 26 | CATGTCACAGTGCCT | H49320 | 23 | 5 | 7 | 11 | 13 | L25081 | Human GTPase (rhoC) mRNA, complete cds. |
| 27 | CATGAATAAAGGCTA | H1031929 | 23 | 5 | 13 | 15 | 25 | D45887 | Human mRNA for calmodulin, complete cds. |
| 28 | CATGTTGTTGTTGAA | H44179 | 23 | 4 | 10 | 16 | 12 | N62815 | yy66b11.s1 Homo sapiens cDNA clone 278493 3'. |
| 29 | CATGAAGGTAGCAGA | H769707 | 21 | 2 | 5 | 14 | 10 | R68633 | yi14b06.s1 Homo sapiens cDNA clone 139187 3'. |
| 30 | CATGGTGTTGGGGGT | H916344 | 21 | 1 | 5 | 7 | 13 | X90858 | H.sapiens mRNA for uridine phosphorylase. |
| 31 | CATGTGCAGCGCCTG | H238697 | 20 | 2 | 4 | 0 | 3 | H19458 | yn54c02.s1 Homo sapiens cDNA clone 172226 3' simil |
| 32 | CATGATGGCACGGAG | H608326 | 20 | 1 | 6 | 1 | 9 | T30468 | EST17149 Homo sapiens cDNA 5' end similar to None. |
| 33 | CATGGCCAGACACCC | H515990 | 20 | 0 | 17 | 3 | 0 | V00491 | Human gene for alpha 1 globin. |
| 34 | CATGCTTCTTGCCCC | H86453 | 19 | 2 | 7 | 22 | 9 | X51345 | Human jun-B mRNA for JUN-B protein. |
| 35 | CATGACCCACGTCAG | H686458 | 18 | 3 | 4 | 5 | 8 | R72429 | yj90e08.s1 Homo sapiens cDNA clone 156038 3'. |
| 36 | CATGGGCTGCCTGCC | | | | | | | R48449 | yj67b10.s1 Homo sapiens cDNA clone 153787 3'. |
| | | | | | | | | R52128 | yj72b03.s1 Homo sapiens cDNA clone 154253 3'. |
| 37 | CATGGAGGGCCGGTG | H567660 | 18 | 2 | 14 | 6 | 16 | X12910 | Human Na+,K+ ATPase gene exons 1 - 3 (alpha III is |
| 38 | CATGGATGAATCCGG | H581847 | 17 | 1 | 3 | 2 | 2 | | Unknown |
| 39 | CATGAGCCCGACCAC | H153109 | 16 | 2 | 11 | 7 | 5 | X81006 | H.sapiens HCG I mRNA. |
| 40 | CATGGTTCAGCTGTC | H774780 | 16 | 2 | 12 | 3 | 12 | L08666 | Homo sapiens porin (por) mRNA, complete cds and tr |
| 41 | CATGCCTCGCTCAGT | H383443 | 16 | 1 | 8 | 6 | 7 | U04627 | Human 78 kDa gastrin-binding protein mRNA, complet |
| 42 | CATGCAAATAAAAGT | H265219 | 15 | 1 | 8 | 9 | 0 | U17077 | Human BENE mRNA, partial cds. |
| 43 | CATGTGCCGCCCGCA | H940378 | 15 | 1 | 8 | 0 | 3 | U28369 | Human semaphorin V mRNA, complete cds. |
| 44 | CATGGCAGTGGCCTC | H601752 | 15 | 0 | 6 | 4 | 3 | D12038 | Human HepG2 3'-directed Mbol cDNA, clone s150. |
| 45 | CATGCTGGGCCTGAA | H502137 | 14 | 0 | 3 | 3 | 18 | U77396 | Human TNF-alpha inducible responsive element mRNA, |
| 46 | CATGGCCCATTGGAG | H611305 | 13 | 1 | 6 | 13 | 17 | Z29093 | H.sapiens EDDR1 gene for receptor tyrosine kinase. |
| 47 | CATGAAGAAAACCTC | H32792 | 12 | 0 | 2 | 2 | 0 | T94990 | ye38a04.s1 Homo sapiens cDNA clone 119982 3'. |
| | | | | | | | | N69310 | za25g05.s1 Homo sapiens cDNA clone 293624 3'. |
| | | | | | | | | | zb86e03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA |
| | | | | | | | | N98502 | clone 310492 3' |
| 48 | CATGGAATGATTTCT | H538878 | 12 | 0 | 6 | 6 | 14 | F18838 | H.sapiens EST sequence (007-X1-01) from skeletal m |
| | | | | | | | | | zr21b10.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens |
| 49 | CATGGCCTGGTCCTT | H621272 | 12 | 0 | 3 | 3 | 8 | AA226928 | cDNA clone 664027 3' |
| 50 | CCATGGCCCACACAG | H610579 | 11 | 0 | 1 | 1 | 0 | M60047 | Human heparin binding protein (HBp17) mRNA |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 51 | CATGGGATTCCAGTT | H671052 | 11 | 0 | 4 | 3 | 2 | W52456 | zc45e09.r1 Soares senescent fibroblasts NbHSF Homo |

# Transcripts decreased in both colon primary tumors and colon cancer cell lines compared to normal colon (130 genes)

NC: Normal Colon
TU: Colon Primary Tumor
CL: Colon Cancer Cell Line
PT: Pancreatic Primary Tumor
PC: Pancreatic Cancer Cell Line

| # | Tag Sequence | Tag_Number | NC | TU | CL | PT | PC | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGCCTCCAGCTAC | H382109 | 803 | 191 | 304 | 136 | 663 | X12882 | Human mRNA for cytokeratin 8. |
| 2 | CATGCTAAGACTTCA | H460926 | 708 | 282 | 402 | 142 | 497 | F15636 | H.sapiens mitochondrial EST sequence (002T15) |
| 3 | CATGGCCCAGGTCAC | H610997 | 705 | 58 | 2 | 2 | 1 | | Unknown |
| 4 | CATGACCCTTGGCCA | H90022 | 512 | 348 | 93 | 43 | 235 | F16940 | H.sapiens mitochondrial EST sequence (009-T1-21) f |
| 5 | CATGACATTGGGTGA | H81583 | 504 | 92 | 4 | 0 | 0 | M10050 | Human liver fatty acid binding protein (FABP) mRNA |
| 6 | CATGGCGAAACCCTG | H622680 | 486 | 108 | 27 | 30 | 13 | S61953 | c-erbB3=receptor tyrosine kinase (alternatively sp |
| 7 | CATGAGCCCTACAAA | H153361 | 367 | 242 | 132 | 71 | 204 | F15506 | H.sapiens mitochondrial EST sequence (1-t-02) from |
| 8 | CATGGACCCAAGATA | H545828 | 276 | 131 | 0 | 7 | 0 | T39321 | ya04c01.r2 Homo sapiens cDNA clone 60480 5'. |
| | | | | | | | | H24673 | yl41a01.s1 Homo sapiens cDNA clone 160776 3'. |
| | | | | | | | | D25586 | HUMGS02706 Human colon 3'directed MboI cDNA, HUMGS02706, clone cm1673. |
| | | | | | | | | T96160 | ye09b02.s1 Homo sapiens cDNA clone 117195 3'. |
| 9 | CATGGCCGGGTGGGC | H617195 | 256 | 88 | 148 | 144 | 178 | X64364 | H.sapiens mRNA for M6 antigen. |
| 10 | CATGTTGGGGTTTCC | H1026814 | 202 | 75 | 84 | 235 | 369 | M11146 | Human ferritin H chain mRNA, complete cds. |
| 11 | CATGCTCCAECCGAA (or G) | H479577 | 201 | 120 | 0 | 11 | 3 | L15203 | Human secretory protein (P1.B) mRNA, complete cds. |
| 12 | CATGGCAGGGCCTCA | H600670 | 196 | 68 | 6 | 32 | 19 | X93036 | H.sapiens mRNA for MAT8 protein. |
| 13 | CATGATCGTGGCGGG | H224923 | 194 | 24 | 97 | 40 | 39 | H93844 | yv07h09.r1 Homo sapiens cDNA clone 242081 5' similar to SP:A39484 A39484 ANDROGEN-WITHDRAWAL APOPTOSIS PROTEIN RVP1, |
| 14 | CATGCAAGCATCCCC | H271574 | 190 | 99 | 101 | 30 | 139 | F17001 | H.sapiens mitochondrial EST sequence (011-T1-13) f |
| 15 | CATGGACATCAAGTC | H544012 | 189 | 33 | 76 | 57 | 219 | Y00503 | Human mRNA for keratin 19. |
| 16 | CATGGTTGTGGTTAA | H782013 | 178 | 110 | 14 | 340 | 139 | W16632 | zb05a11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301148 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);. |
| | | | | | | | | AA143804 | zo31h04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588535 3' |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | AA133597 | 97 zl92h02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 512115 3 |
| | | | | | | | | T53199 | ya86c05.s1 Homo sapiens cDNA clone 68552 3'. |
| 17 | CTAGTGCTCCTACCC | H947654 | 174 | 27 | 1 | 0 | 0 | R00081 | ye73c04.s1 Homo sapiens cDNA clone 123366 3'. |
| 18 | CATGCACCCCTGATG | H284132 | 172 | 33 | 26 | 3 | 6 | M16364 | Human creatine kinase-B mRNA, complete cds. |
| 19 | CATGCCGCTGCACTC | H368200 | 163 | 40 | 4 | 10 | 4 | R09410 | yf22e12.s1 Homo sapiens cDNA clone 127630 3' similar to contains Alu repetitive element |
| | | | | | | | | C01918 | HUMGS0003915, Human Gene Signature, 3'-directed cDNA sequence. |
| | | | | | | | | R92735 | yq04h09.s1 Homo sapiens cDNA clone 196001 3' similar to contains Alu repetitive element |
| | | | | | | | | W90374 | zh78e12.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone 418222 3' similar to contains Alu repetitive element |
| 20 | CATGCTGGCCCTCGG | H501111 | 163 | 20 | 0 | 26 | 1 | X52003 | H.sapiens pS2 protein gene. |
| 21 | CATGCCCCCTGGATC | H350116 | 160 | 40 | 24 | 88 | 181 | M18981 | Human prolactin receptor-associated protein (PRA) |
| 22 | CATGTTCACTGTGAG | H1001401 | 160 | 34 | 13 | 74 | 71 | M64303 | Human galactoside-binding protein mRNA. |
| 23 | CATGATTGGAGTGCT | H256186 | 155 | 34 | 1 | 11 | 6 | X16455 | Human mRNA for carcinoembryonic antigen pCEA80-11. |
| 24 | CATGCTGACCTGTGT | H493039 | 149 | 44 | 32 | 98 | 37 | U14943 | Human MHC antigen (HLA-B) mRNA, complete cds. |
| 25 | CATGAGCAGATCAGG | H149715 | 145 | 50 | 88 | 156 | 130 | M81457 | Human calpactin I light chain mRNA, complete cds. |
| 26 | CATGGGAAAACAGAA | H655433 | 126 | 37 | 0 | 24 | 16 | C21047 | HUMGS0002546, Human Gene Signature, 3'-directed cDNA sequence |
| | | | | | | | | AA132779 | zo21h08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587583 3' similar to SW:LEG4_RAT P38552 GALECTIN-4 |
| | | | | | | | | AA054072 | zl68h06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509819 3' |
| | | | | | | | | AA132736 | zo18g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587294 3' similar to SW:LEG4_RAT P38552 GALECTIN-4 |
| 27 | CATGTCACCGGTCAG | H857781 | 122 | 7 | 7 | 30 | 7 | X04412 | Human mRNA for plasma gelsolin. |
| 28 | CATGTGCAGCACGAG | H936217 | 122 | 26 | 32 | 84 | 2 | X77658 | H. sapiens mRNA for HLA-B*7301. |
| 29 | CATGGGAACTGTGAA | H657337 | 115 | 7 | 1 | 14 | 21 | AA146606 | zo35c09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588880 3' |
| | | | | | | | | AA146775 | zo35g09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588928 3' |
| | | | | | | | | AA161043 | zo74g11.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592676 3' |

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|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | AA088704 | zl83f08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511239 3' |
| 30 | CATGCGAGGGGCCAG | H404117 | 114 | 32 | 54 | 60 | 40 | H00427 | yj23g11.r1 Homo sapiens cDNA clone 149636 5'. |
| | | | | | | | | AA158715 | zo63d03.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 591557 3' |
| | | | | | | | | T08562 | EST06454 Homo sapiens cDNA clone HIBBG31 3' end. |
| | | | | | | | | AA078845 | zm21a12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526270 3' |
| 31 | CATGTAAATTGCAAA | H790417 | 113 | 6 | 1 | 0 | 0 | X73502 | H..Sapiens mRNA for cytokeratin 20. |
| 32 | CATGGGCTGGGGGCC | H686762 | 113 | 36 | 48 | 45 | 43 | J03191 | Human profilin mRNA, complete cds. |
| 33 | CATGGTGCTGAATGG | H761359 | 109 | 20 | 30 | 67 | 111 | U02629 | Human smooth muscle myosin alkali light chain mRNA |
| 34 | CATGGTGCACTGAGC | H758243 | 107 | 13 | 36 | 34 | 82 | X07059 | Human M4-50 mRNA for HLA class I antigen. |
| 35 | CATGTTTAACGGCCG | H1032614 | 107 | 31 | 14 | 3 | 37 | F15592 | H.sapiens mitochondrial EST sequence (001T24) from |
| 36 | CATGCCCTCCCGAAG | H357729 | 106 | 17 | 7 | 3 | 6 | AA053660 | zl74e07.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510372 3' similar to contains Alu repetitive element |
| | | | | | | | | D25711 | HUMGS04077 Human colon 3'directed MboI cDNA, HUMGS04077, clone cm1210 |
| 37 | CATGAGGTGGCAAGA | H178755 | 105 | 15 | 22 | 14 | 27 | Z56800 | H.sapiens CpG DNA, clone 140c4, reverse read cpg14(Mitochondria EST |
| 38 | CATGATACTCCACTC | H204104 | 102 | 11 | 0 | 0 | 0 | M95174 | Human guanylin mRNA, complete cds. |
| 39 | CATGCTCGCGCTGGG | H484987 | 101 | 25 | 5 | 4 | 16 | | Unknown |
| 40 | CATGGGGGCAGGGCC | H697514 | 82 | 32 | 28 | 37 | 65 | R90863 | yn01b01.r1 Homo sapiens cDNA clone 167113 5' similar to SP:ZK783.1 CE00760 ;. |
| | | | | | | | | T24702 | EST277 Homo sapiens cDNA clone 10H4. |
| 41 | CATGGAAGCAGGACC | H533666 | 80 | 33 | 42 | 28 | 87 | X95404 | H.sapiens mRNA for non-muscle type cofilin. |
| 42 | CATGCCAGGGGAGAA | H338569 | 75 | 22 | 28 | 30 | 16 | X67325 | H.sapiens p27 mRNA. |
| 43 | CATGACACAGCAAGA | H70211 | 74 | 31 | 30 | 10 | 31 | F16604 | H.sapiens mitochondrial EST sequence (009T28) from |
| 44 | CATGAGAATAGCTTG | H134304 | 69 | 29 | 1 | 3 | 0 | N69361 | za16a03.s1 Homo sapiens cDNA clone 292684 3' similar to contains Alu repetitive element;contains element L1 repetitive element |
| | | | | | | | | AA015918 | ze30b10.s1 Soares retina N2b4HR Homo sapiens cDNA clone 360475 3' similar to contains Alu repetitive element |
| | | | | | | | | H26689 | yl14h01.s1 Homo sapiens cDNA clone 158257 3' similar to contains Alu repetitive element;contains TAR1 repetitive element ;. |
| 45 | CATGCGCTGTGGGGT | H424875 | 68 | 9 | 6 | 5 | 23 | AA256365 | zr79h11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681957 3' similar to WP:C33A12.7 CE05353 |

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|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | W47357 | zc39e11.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324716 3' |
| | | | | | | | | W19276 | zb90f03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 310877 3' |
| | | | | | | | | R07159 | yf13h12.s1 Homo sapiens cDNA clone 126791 3'. |
| 46 | CATGCATAGGTTTAG | H314109 | 68 | 5 | 0 | 0 | 0 | L02785 | Homo sapiens colon mucosa-associated (DRA) mRNA |
| 47 | CATGGCCGACCAGGT | H614731 | 65 | 19 | 0 | 3 | 6 | U11862 | Human clone HP-DAO1 diamine oxidase |
| 48 | CATGAGCTCTTGGAG | H161769 | 64 | 11 | 1 | 1 | 2 | N93240 | zb68b06.s1 Homo sapiens cDNA clone 308723 3'. |
| | | | | | | | | T16906 | NIB1986 Normalized infant brain, Bento Soares Homo sapiens cDNA 3'end. |
| | | | | | | | | H78256 | yu22h07.s1 Homo sapiens cDNA clone 234589 3' similar to SP:SBP_MOUSE P17563 SELENIUM-BINDING |
| | | | | | | | | T32362 | EST47523 Homo sapiens cDNA 3'.end similar to similar to Selenium-binding protein,liver. |
| 49 | CATGCCCAACGCGCT | H344474 | 57 | 1 | 0 | 3 | 0 | V00493 | Human messenger RNA for alpha globin. |
| 50 | CATGGACGCGGCGCG | H550554 | 55 | 21 | 2 | 7 | 14 | | Unknown |
| 51 | CATGACCCCCCCGCC | H87386 | 54 | 16 | 15 | 15 | 3 | X51346 | Human jun-D mRNA for JUN-D protein. |
| 52 | CATGATGCGGGAGAA | H236169 | 52 | 6 | 10 | 11 | 7 | R34039 | yh83f04.r1 Homo sapiens cDNA clone 136351 5'. |
| | | | | | | | | H03961 | yj44e07.s1 Homo sapiens cDNA clone 151620 3'. |
| | | | | | | | | R33498 | yh83f04.s1 Homo sapiens cDNA clone 136351 3'. |
| 53 | CATGTCAGCTGCAAC | H862097 | 51 | 6 | 0 | 0 | 0 | AA053043 | zl71e06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 510082 5' |
| 54 | CATGGTAAGTGTACT | H723890 | 50 | 14 | 15 | 1 | 30 | F17394 | H.sapiens mitochondrial EST sequence (007T13) from |
| 55 | CATGTGTGGGTGCTG | H977640 | 49 | 20 | 17 | 21 | 8 | Z13009 | H.sapiens mRNA for E-cadherin. |
| 56 | CATGGCTGTGCCTGG | H650847 | 48 | 17 | 15 | 8 | 31 | X15505 | Human mRNA for pancreatic trypsinogen III. |
| 57 | CATGTGAGTGACAGA | H929299 | 48 | 4 | 0 | 0 | 0 | H14641 | yl26g02.s1 Homo sapiens cDNA clone 159410 3'. |
| 58 | CATGGGCTGGGCCTG | H686744 | 47 | 11 | 13 | 32 | 8 | M20469 | Human brain-type clathrin light-chain b mRNA, |
| 59 | CATGTAATCCCAGCA | H800074 | 46 | 15 | 5 | 8 | 11 | N50873 | yy92c07.s1 Homo sapiens cDNA clone 281004 3' similar to contains Alu repetitive element;contains element MER32 repetitive element |
| 60 | CATGGACCAGTGGCT | H545514 | 45 | 1 | 0 | 0 | 1 | U79725 | Human A33 antigen precursor mRNA, complete cds |
| 61 | CATGGGCACCGTGCT | H673210 | 44 | 10 | 1 | 14 | 14 | | Unknown |
| 62 | CATGAAGGACCTTTT | H41344 | 43 | 17 | 14 | 22 | 24 | H11216 | ym14f06.r1 Homo sapiens cDNA clone 47991 5'. |
| | | | | | | | | H52178 | yt85h08.s1 Homo sapiens cDNA clone 231135 3'. |
| | | | | | | | | T40539 | ya05b02.s1 Homo sapiens cDNA clone 60555 3'. |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | AA303091 | EST12940 Uterus tumor I Homo sapiens cDNA 3' end | |
| 63 | CATGGCAGCTCCTGT | H599903 | 43 | 8 | 17 | 24 | 13 | W02429 | za52d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 296163 5'. | |
| | | | | | | | | N20325 | yx44c11.s1 Homo sapiens cDNA clone 264596 3'. | |
| | | | | | | | | N45127 | yz13c12.s1 Homo sapiens cDNA clone 282934 3'. | |
| | | | | | | | | N90407 | zb38c11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305876 3'. | |
| 64 | CATGTGTCCTGGTTC | H972720 | 43 | 12 | 14 | 25 | 5 | U03106 | Human wild-type p53 activated fragment-1 (WAF1) mR | |
| 65 | CATGACAAACCCCCA | H65878 | 42 | 16 | 7 | 12 | 11 | W37827 | zc11f01.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322009 3' | |
| | | | | | | | | W15332 | gb\|W15332\|W15332 zc16d10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322483 3' | |
| | | | | | | | | W32410 | zc04g10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321378 3' | |
| | | | | | | | | N32312 | yw82c01.s1 Homo sapiens cDNA clone 258720 3'. | |
| 66 | CATGTAGGATGGGGG | H828331 | 41 | 6 | 11 | 6 | 9 | U51478 | Human sodium/potassium-transporting ATPase beta-3 | |
| 67 | CATGACTGTGGCGGC | H126619 | 41 | 7 | 1 | 4 | 35 | | Unknown | |
| 68 | CATGGTAGCAGGTGT | H730287 | 40 | 7 | 13 | 17 | 24 | AA180815 | zp44f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 612333 3' similar to contains Alu repetitive element; | |
| | | | | | | | | R34696 | yh87e04.s1 Homo sapiens cDNA clone 136734 3' similar to contains Alu repetitive element; | |
| | | | | | | | | R34696 | yh87e04.s1 Homo sapiens cDNA clone 136734 3' similar to contains Alu repetitive element; | |
| | | | | | | | | AA194497 | zq06e03.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 628924 3' similar to contains Alu repetitive element | |
| 69 | CATGAATCACAAATA | H53508 | 40 | 12 | 0 | 3 | 0 | T11144 | hbc760 Homo sapiens cDNA clone hbc760 3'end similar to nonspacific crossreacting antigen. | |
| | | | | | | | | AA058357 | zl67e01.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509688 3' similar to TR:G189087 | |
| | | | | | | | | C05803 | similar to none | |
| | | | | | | | | AA143765 | zo31e02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588506 3' | |
| 70 | CATGAGGATGGTCCC | H167606 | 40 | 11 | 4 | 4 | 5 | | zp45b09.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone | |
| | | | | | | | | AA179299 | 612377 3' | |

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|---|---|---|---|---|---|---|---|---|---|
| 71 | CATGCCAAAGCTATA | H328308 | 38 | 11 | 6 | 2 | 18 | M35252 | Human CO-029. |
| 72 | CATGCGGGAGTCGGG | H434907 | 38 | 8 | 6 | 0 | 0 | R87448 | ym89c10.s1 Homo sapiens cDNA clone 166098 3'. |
| 73 | CATGGCCGTGGAGAG | H618121 | 38 | 9 | 5 | 17 | 26 | X79882 | H.sapiens lrp mRNA. |
| 74 | CATGCCCCCGAAGCC | H349706 | 37 | 6 | 0 | 0 | 0 | | Unknown |
| 75 | CATGATTTCAAGATG | H259108 | 37 | 1 | 0 | 0 | 0 | J03037 | Human carbonic anhydrase II mRNA, complete cds. |
| 76 | CATGGCCCAGTGGCT | H611050 | 37 | 3 | 0 | 2 | 10 | | Unknown |
| 77 | CATGATGGTGGGGGA | H241323 | 36 | 2 | 6 | 25 | 2 | M92843 | H.sapiens zinc finger transcriptional regulator mRNA |
| 78 | CATGCCTGCCCCCCT | H386390 | 35 | 12 | 7 | 7 | 5 | X60188 | Human ERK1 mRNA for protein serine/threonine kinase |
| 79 | CTAGTGGAAAGTGAA | H950457 | 34 | 1 | 1 | 12 | 0 | V01512 | Human cellular oncogene c-fos (complete sequence). |
| 80 | CATGGTCATCACCAC | H740629 | 34 | 0 | 0 | 0 | 0 | U34279 | Human uroguanylin mRNA, complete cds. |
| 81 | CATGCTTATGGTCCC | H511670 | 34 | 1 | 0 | 3 | 1 | AA287021 | zs57c03.s1 Soares NbHTGBC Homo sapiens cDNA clone 701572 3' |
| 82 | CATGCTGGGCCTCTG | H502136 | 34 | 3 | 4 | 11 | 5 | T55226 | yb47a01.s1 Homo sapiens cDNA clone 74280 3' containing L1 repetitive element |
| | | | | | | | | R37446 | yf56e10.s1 Homo sapiens cDNA clone 26129 3' similar to gb:X07173 INTER-ALPHA-TRYPSIN INHIBITOR COMPLEX COMPONENT II |
| | | | | | | | | AA406180 | zu65c08.s1 Soares testis NHT Homo sapiens cDNA clone 742862 3' |
| 83 | CATGGCCCAGGGCCC | H610982 | 33 | 3 | 0 | 0 | 2 | R09752 | Unknown |
| 84 | CATGTTTTTACTGAT | H1047673 | 33 | 7 | 0 | 4 | 2 | R81530 | yj02b10.r1 Homo sapiens cDNA clone 147547 5'. |
| | | | | | | | | T32348 | EST47211 Homo sapiens cDNA 3' end similar to None.. |
| | | | | | | | | W57810 | zd17g02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340946 3' |
| | | | | | | | | AA398527 | zt47e12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725518 3' |
| 85 | CATGCCTGCTTGTCG | H387054 | 32 | 2 | 1 | 6 | 32 | X63187 | H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue |
| 86 | CATGACCTGGGGAGG | H96931 | 32 | 6 | 4 | 8 | 6 | | Unknown |
| 87 | CATGCCTTCAAATCA | H390158 | 31 | 1 | 0 | 0 | 0 | R46266 | yg52g07.s1 Homo sapiens cDNA clone 36232 3' similar to gb:M33987 CARBONIC ANHYDRASE I |
| 88 | CATGTCGGAGCTGTT | H893564 | 30 | 1 | 4 | 7 | 1 | H98618 | yx12a06.s1 Homo sapiens cDNA clone 261490 3'. |
| | | | | | | | | AA171705 | zo97h01.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594865 3' |
| | | | | | | | | H99212 | yx15g08.s1 Homo sapiens cDNA clone 261854 3'. |

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|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | AA029975 | zk10e12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470158 3' |
| 89 | CATGGGAGGTGGGGC | H666539 | 30 | 6 | 5 | 32 | 22 | M75161 | H.sapiens granulin mRNA, complete cds |
| 90 | CATGTTCCACTAACC | H1003970 | 30 | 7 | 3 | 16 | 17 | T30344 | gb\|U53204\|HSU53204 Human plectin (PLEC1) mRNA, complete cds. |
| 91 | CATGGTCTGGGGGAT | H752297 | 29 | 1 | 3 | 9 | 3 | T60135 | yc22a06.s1 Homo sapiens cDNA clone 81394 3'. |
| | | | | | | | | T30403 | gb\|U67963\|HSU67963 Human lysophospholipase homolog (HU-K5) mRNA |
| 92 | CATGTTAACCCCTCC | H984414 | 29 | 5 | 0 | 18 | 0 | R23595 | yh39a12.r1 Homo sapiens cDNA clone 132094 5' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN) |
| | | | | | | | | R69445 | yj83c08.s1 Homo sapiens cDNA clone 155342 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);. |
| | | | | | | | | R79191 | yi84h01.s1 Homo sapiens cDNA clone 145969 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);. |
| | | | | | | | | R49965 | yj56c03.s1 Homo sapiens cDNA clone 152740 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);. |
| 93 | CATGATGACGCTCAC | H231029 | 28 | 5 | 5 | 4 | 6 | AA410947 | zv35h12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755687 5' similar to TR:G459890 G459890 OVEREXPRESSED IN TESTICULAR TUMORS |
| | | | | | | | | H02520 | yj40c11.r1 Homo sapiens cDNA clone 151220 5'. |
| | | | | | | | | AA130551 | zo12g08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 586718 5' similar to TR:G459890 G459890 OVEREXPRESSED IN TESTICULAR TUMORS. |
| | | | | | | | | | |
| 94 | CATGCACCTGTCATC | H286420 | 28 | 5 | 0 | 5 | 4 | W68230 | zd33c10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342450 3' similar to contains Alu repetitive element |
| | | | | | | | | R89822 | yp90a02.s1 Homo sapiens cDNA clone 194666 3' similar to contains Alu repetitive element; |
| | | | | | | | | AA053322 | zk69e08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488102 3' similar to contains element MER6 repetitive element |
| 95 | CATGGATCCCAACTG | H578824 | 27 | 1 | 1 | 24 | 17 | V00594 | Human mRNA for metallothionein from cadmium-treated cells |
| 96 | CATGCTTAGAGGGGT | H510123 | 27 | 1 | 5 | 9 | 6 | H43742 | yp21d05.r1 Homo sapiens cDNA clone 188073 5' similar to gb:J05021 EZRIN |
| 97 | CATGATGGCCCATAC | H238925 | 27 | 4 | 3 | 1 | 0 | | emb\|Y09616\|HSICE H.sapiens mRNA for putative carboxylesterase |
| 98 | CATGGCAAGAAAGTG | H591884 | 27 | 1 | 0 | 2 | 0 | V00497 | Human messenger RNA for beta-globin. |

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|---|---|---|---|---|---|---|---|---|---|
| 99 | CATGTACCTCTGATT | H810468 | 27 | 5 | 7 | 11 | 12 | X65614 | H.sapiens mRNA for calcium-binding protein S100P. |
| 100 | CATGATGATGGCACC | H233106 | 26 | 0 | 2 | 0 | 2 | | |
| 101 | CATGTTCTGTAGCCC | H1014566 | 25 | 5 | 0 | 4 | 0 | | emb\|Z69881\|HSSERCA3M H.sapiens mRNA for adenosine triphosphatase, calcium |
| 102 | CATGCCTGTCTGCCA | H388582 | 24 | 1 | 2 | 1 | 3 | T99568 | ye65c02.r1 Homo sapiens cDNA clone 122594 5'. |
| | | | | | | | | T87539 | yd89f09.s1 Homo sapiens cDNA clone 115433 3'. |
| 103 | CATGTATGATGAGCA | H844682 | 23 | 4 | 0 | 1 | 0 | | gb\|AA347726\|AA347726 EST54132 Fetal heart II Homo sapiens cDNA 5' end similar to transmembrane secretory component |
| 104 | CATGCTGGCAAAGGT | H500747 | 23 | 0 | 0 | 0 | 0 | | |
| 105 | CATGCTTGATTCCCA | H517078 | 23 | 4 | 4 | 17 | 7 | L42379 | Homo sapiens bone-derived growth factor (BPGF-1) m |
| 106 | CATGCTTGACATACC | H516402 | 22 | 0 | 0 | 7 | 2 | X68277 | H.sapiens CL 100 mRNA for protein tyrosine phosphase |
| 107 | CATGGCTGGCACATT | H649492 | 22 | 5 | 0 | 0 | 0 | M82962 | Human N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase alpha subunit (PPH alpha) mRNA, complete cds |
| 108 | CATGTCTGAATTATG | H909556 | 21 | 1 | 1 | 1 | 1 | X16354 | Human mRNA for transmembrane carcinoembryonic antigen (CEA) |
| 109 | CATGGGAAGAGCACT | H657554 | 21 | 1 | 1 | 3 | 3 | X74570 | H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAcalpha-2,3-sialyltransferase |
| 110 | CATGGCTCTTCCCCA | H646998 | 20 | 2 | 0 | 1 | 0 | R87768 | yo45d01.s1 Homo sapiens cDNA clone 180865 3' similar to contains PTR5 repetitive element |
| | | | | | | | | R85880 | yo36g07.s1 Homo sapiens cDNA clone 180060 3' similar to contains PTR5 repetitive element |
| 111 | CATGAAATCTGGCAC | H14245 | 20 | 2 | 0 | 4 | 3 | L20826 | Human I-plastin mRNA, complete cds. |
| 112 | CATGTAATTTGCATT | H802708 | 19 | 2 | 0 | 1 | 7 | Z50751 | HSB4BMR H.sapiens mRNA for B4B |
| | | | | | | | | U77085 | Human epithelial membrane protein (CL-20) mRNA, complete cds |
| | | | | | | | | Y07909 | HSPAPR H.sapiens mRNA for Progression Associated Protein |
| 113 | CATGGTGGGGGCGCC | H764570 | 18 | 1 | 1 | 8 | 2 | R48529 | yj64g10.r1 Homo sapiens cDNA clone 153570 5'. |
| 114 | CATGTTATGGTGTGA | H998127 | 17 | 0 | 0 | 1 | 0 | T27534 | EST10a24 Clontech adult human fat cell library HL1108A Homo sapiens cDNA clone 10a24. |
| 115 | CATGGGAGAAACAGC | H663571 | 17 | 1 | 2 | 4 | 0 | T86124 | yd84b04.s1 Homo sapiens cDNA clone 114895 3'. |
| | | | | | | | | AA131008 | zo15g05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587000 3' |
| | | | | | | | | R49945 | yj58g11.s1 Homo sapiens cDNA clone 152996 3'. |
| | | | | | | | | T57044 | ya84h01.s1 Homo sapiens cDNA clone 68401 3'. |
| 116 | CATGCCAACACCAGC | H328787 | 17 | 1 | 0 | 0 | 0 | | |
| 117 | CATGAGGTGACTGGG | H178299 | 17 | 0 | 0 | 0 | 0 | | |
| 118 | CATGGCCATCCTCCA | H609654 | 16 | 0 | 0 | 0 | 0 | | gb\|R73013\|R73013 yj94a09.r1 Homo sapiens cDNA clone 156376 5'. |

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|---|---|---|---|---|---|---|---|---|---|
| 119 | CATGTTTCTCGTCGC | H1039799 | 15 | 1 | 0 | 4 | 4 | M69013 | Human guanine nucleotide-binding regulatory protein |
| 120 | CATGTCAGAGCGCTG | H860776 | 15 | 1 | 1 | 1 | 0 | | Unknown |
| 121 | CATGTTCCGCGTTCC | H1006014 | 14 | 1 | 0 | 0 | 2 | N58523 | yv72h06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 248315 3' similar to contains element PTR7 repetitive element |
| 122 | CATGTACGGTGTGGG | H814011 | 14 | 1 | 0 | 0 | 0 | | Unknown |
| 123 | CATGCTCAGAACTTG | H477216 | 14 | 0 | 1 | 4 | 13 | | Unknown |
| 124 | CATGGGACTAAATGA | H662543 | 13 | 1 | 0 | 1 | 0 | M29540 | Human carcinoembryonic antigen mRNA (CEA), complete cds. |
| 125 | CATGGCTTGGGGATT | H653988 | 12 | 0 | 0 | 0 | 1 | D25786 | HUMGS04154 Human colon 3'directed MboI cDNA, HUMGS04154, clone cm0215. |
| | | | | | | | | T73613 | yc36e02.r1 Homo sapiens cDNA clone 82778 5' similar to gb:L07765 LIVER CARBOXYLESTERASE PRECURSOR |
| 126 | CATGACCCAACTGCC | H86138 | 12 | 0 | 0 | 0 | 1 | | Unknown |
| 127 | CATGCTGAACCTCCC | H491894 | 12 | 0 | 0 | 2 | 2 | | gb\|T95615\|T95615 ye40e03.s1 Homo sapiens cDNA clone 120220 3'. |
| 128 | CATGCAAGAGTTTCT | H271102 | 11 | 0 | 0 | 2 | 0 | AA226797 | zr19b11.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 663837 3' |
| | | | | | | | | AA218730 | zq97h01.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 649969 3' |
| 129 | CATGGTCCGAGTGCA | H743610 | 11 | 0 | 0 | 8 | 5 | H38178 | yp57f10.r1 Homo sapiens cDNA clone 191563 5' similar to gb:M90657 TUMOR-ASSOCIATED ANTIGEN L6 (HUMAN);. |
| 130 | CATGTTTGGTTTCAC | H1043445 | 11 | 0 | 0 | 0 | 0 | | Unknown |

# Transcripts decreased in only colon cancer cell lines compared to normal colon (78 genes)

NC Normal Colon
TU Colon Primary Tumor
CL Colon Cancer Cell Line
PT Pancreatic Primary Tumor
PC Pancreatic Cancer Cell Line

| # | Tag sequence | Tag_Number | NC | TU | CL | PT | PC | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGCACCTAATTGG | H285759 | 612 | 755 | 411 | 161 | 333 | F15516 | H.saplens mitochondrial EST sequence (1-t-12) |
| 2 | CATGATTTGAGAAGC | H260227 | 603 | 566 | 158 | 249 | 173 | F12396 | H. sapiens partial cDNA sequence; clone c-39e04. |
| 3 | CATGTGATTTCACTT | H933704 | 452 | 595 | 235 | 80 | 314 | L08441 | Human autonomously replicating sequence (ARS) mRNA |
| 4 | CATGTTCATACACCT | H1002566 | 444 | 357 | 114 | 64 | 191 | F15553 | H.sapiens mitochondrial EST sequence (001T14) |
| 5 | CATGCCACTGCACTC | H335432 | 385 | 402 | 223 | 278 | 132 | X51525 | Human cortex mRNA containing an Alu repetitive element |
| 6 | CATGACTAACACCCT | H114966 | 369 | 446 | 171 | 76 | 161 | F16402 | H.sapiens mitochondrial EST sequence (141-20) |
| 7 | CATGCACTACTCACC | H291282 | 293 | 527 | 78 | 14 | 83 | U09500 | Human mitochondrion cytochrome b gene, partial cds |
| 8 | CATGAAAACATTCTC | H1272 | 200 | 169 | 98 | 17 | 223 | F15744 | H.sapiens mitochondrial EST sequence (101-03) |
| 9 | CATGCTCATAAGGAA | H478249 | 184 | 127 | 70 | 21 | 75 | F15511 | H.sapiens mitochondrial EST sequence (1-t-07) |
| 10 | CATGTCGAAGCCCCC | H885334 | 147 | 183 | 94 | 49 | 57 | F18587 | H.sapiens mitochondrial EST sequence (022T19) |
| 11 | CATGACGCAGGGAGA | H103075 | 145 | 160 | 91 | 69 | 47 | H03983 | yj47a08.s1 Homo sapiens cDNA clone 151862 3'. |
| 12 | CATGTTGGCCAGGCT | H1025322 | 124 | 194 | 63 | 111 | 51 | X74301 | H.sapiens mRNA for MHC class II transactivator. |
| 13 | CATGTTGGTGAAGGA | H1027595 | 98 | 106 | 17 | 183 | 107 | M17733 | Human thymosin beta-4 mRNA, complete cds. |
| 14 | CATGATCACGCCCTC | H214616 | 97 | 186 | 17 | 41 | 49 | U46913 | Human EST overexpressed in pancreatic cancer (xs31) |
| 15 | CATGTGCCTGCACCA | H941638 | 67 | 48 | 25 | 75 | 34 | X05607 | Human mRNA for cysteine proteinase inhibitor precursor |
| 16 | CATGAGACCCACAAC | H136465 | 64 | 121 | 28 | 24 | 15 | D54113 | Human fetal brain cDNA 5'-end GEN-129B05. |
| 17 | CATGAGTTTGTTAGT | H196339 | 60 | 33 | 17 | 13 | 15 | X14758 | Human mRNA for adenocarcinoma-associated antigen |
| 18 | CATGGGAACAAACAG | H656389 | 56 | 41 | 4 | 31 | 3 | L33930 | Homo sapiens CD24 signal transducer mRNA |
| 19 | CATGTGGTGTATGCA | H965434 | 53 | 271 | 6 | 30 | 5 | D50954 | Human fetal brain cDNA 3'-end GEN-002A10. |
| 20 | CATGGAAATACAGTT | H527436 | 49 | 35 | 10 | 100 | 36 | M11233 | Human cathepsin D mRNA, complete cds. |
| 21 | CATGGTGGCTCACGC | H763719 | 49 | 37 | 21 | 27 | 15 | U25801 | Human Tax1 binding protein mRNA, partial cds. |
| 22 | CATGGTGGTGCACAC | H765509 | 45 | 26 | 18 | 23 | 15 | U31215 | Human metabotropic glutamate receptor 1 alpha |
| 23 | CATGGGGTTGGCTTG | H704160 | 44 | 56 | 2 | 6 | 1 | S79597 | tRNASer(UNC) [human, muscle, MERRF/MELAS overlap s |
| 24 | CATGGTGGCGGGTGC | H763567 | 42 | 32 | 15 | 20 | 5 | T48809 | yb05c03.r1 Homo sapiens cDNA clone 70276 5' contai |
| 25 | CATGTAGACTAGCAA | H821029 | 39 | 23 | 1 | 23 | 10 | M69023 | Human globin gene. |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 26 | CATGGCTAGGTTTAT | H641789 | 38 | 144 | 13 | 25 | 13 | D51017 | Human fetal brain cDNA 3'-end QEN-007C04. |
| 27 | CATGGGCTTTAGGGA | H687915 | 37 | 372 | 6 | 29 | 11 | W15552 | zb91h11.s1 Soares parathyroid tumor NbHPA Homo sap |
| 28 | CATGGGGGTCAGGG | H699691 | 37 | 170 | 11 | 16 | 9 | F16326 | H.sapiens mitochondrial EST sequence (132-20) from skeletal muscle |
| 29 | CATGATTTTCTAAAA | H261569 | 33 | 13 | 11 | 8 | 2 | AA315049 | EST186995 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end |
| 30 | CATGCACTTGCCCT | H294488 | 33 | 18 | 11 | 17 | 36 | F01150 | H. sapiens partial cDNA sequence; clone A6A03; ver |
| 31 | CATGCCTGCTGCAGG | H386963 | 32 | 13 | 0 | 6 | 2 | N29971 | yw53h01.s1 Homo sapiens cDNA clone 255985 3'. |
| 32 | CATGAGAACCTTCCA | H132598 | 32 | 14 | 3 | 16 | 12 | K02883 | Human MHC class I HLA-A2 gene, complete cds. |
| 33 | CATGCTCTGCCCTC | H489822 | 32 | 32 | 7 | 20 | 5 | R09140 | yf25f12.s1 Homo sapiens cDNA clone 127919 3'. |
| | | | | | | | | R76005 | yl22c10.s1 Homo sapiens cDNA clone 158994 3'. |
| | | | | | | | | T33596 | EST58371 Homo sapiens cDNA 3' end similar to None.. |
| 34 | CATGGCCATCCCCTT | H609624 | 29 | 73 | 7 | 14 | 16 | F16449 | H.sapiens mitochondrial EST sequence (129-09) |
| 35 | CATGGCCCAGCGGCC | H610922 | 28 | 9 | 1 | 1 | 7 | AA292959 | zt54f10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726187 3' |
| 36 | CATGTGGCGCGTGTC | H956860 | 26 | 8 | 1 | 1 | 2 | AA292466 | zt31c11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 723956 5' similar to TR:G205858 G205858 RAT ORF |
| | | | | | | | | N92384 | zb62d07.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308173 3' similar to PIR:A39484 A39484 androgen-withdrawal apoptosis protein RVP1, prostatic - rat |
| | | | | | | | | N80203 | zb19c06.s1 Homo sapiens cDNA clone 302506 3' similar to PIR:A39484 A39484 androgen-withdrawal apoptosis protein RVP1, prostatic - rat ; |
| | | | | | | | | AA039323 | zk39d06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485195 3' similar to PIR:A39484 A39484 androgen-withdrawal apoptosis protein RVP1 |
| 37 | CATGAGGGTGTTTTC | H175872 | 26 | 218 | 7 | 20 | 10 | U21468 | Human partial cDNA sequence with CCA repeat region |
| 38 | CATGCCTGGGAAGTG | H387596 | 25 | 10 | 0 | 45 | 17 | M34088 | Human episialin variant A mRNA, 3' end. |
| 39 | CATGAGTCTGCTGGA | H188027 | 24 | 9 | 1 | 0 | 0 | | Unknown |
| 40 | CATGCCCGCCTCTTC | H353760 | 24 | 11 | 2 | 3 | 4 | T10098 | seq816 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft |
| 41 | CATGAAAAGAGTGGT | H2235 | 22 | 9 | 2 | 0 | 7 | X83228 | H.sapiens mRNA for LI-cadherin. |
| 42 | CATGGCCACGTGGAG | H607977 | 21 | 7 | 1 | 2 | 2 | L27415 | Homo sapiens huntingtin (HD) gene, exon 66. |
| 43 | CATGAGGATGTGGG | H167659 | 21 | 5 | 4 | 1 | 3 | C00470 | dbj\|C00470\|C00470 HUMGS0007620, Human Gene Signature, 3'-directed cDNA sequence. |
| | | | | | | | | N63531 | yy62g08.s1 Homo sapiens cDNA clone 278174 3'. |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | AA165679 | zo80f04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 593215 3' |
| 44 | CATGTATAGTCCTCT | H838494 | 20 | 7 | 1 | 3 | 4 | AA411012 | zv40a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756074 3' |
| | | | | | | | | AA133595 | zl92g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 512126 3' |
| | | | | | | | | AA292774 | zt56b12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726335 3' |
| 45 | CATGGGTCCTCTCTT | H710520 | 20 | 7 | 2 | 2 | 2 | R53216 | yj73h02.r1 Homo sapiens cDNA clone 154419 5' simil |
| 46 | CATGATGGGCTTGAT | H240121 | 19 | 4 | 0 | 3 | 3 | D20113 | Human HL60 3'directed MboI cDNA, HUMGS01086, clone |
| 47 | CATGCTGCCCCCCAT | H496981 | 19 | 5 | 0 | 1 | 4 | | Unknown |
| 48 | CATGTTCTCTACACA | H1013522 | 19 | 4 | 1 | 8 | 2 | U35048 | Human TSC-22 protein mRNA, complete cds. |
| 49 | CATGAAGAAGCAGGG | H33355 | 18 | 4 | 2 | 2 | 8 | R81767 | yj05g03.r1 Homo sapiens cDNA clone 147892 5'. |
| 50 | CATGAGTAGGTGGCC | H183018 | 18 | 131 | 2 | 17 | 7 | D51021 | Human fetal brain cDNA 3'-end GEN-007D07. |
| 51 | CATGACAGTGTGTGT | H77551 | 18 | 5 | 3 | 0 | 8 | D26146 | Human DNA for putative protein kinase. |
| 52 | CATGGGAAAAGTGGT | H655547 | 18 | 13 | 3 | 70 | 1 | M11465 | Human alpha-1-antitrypsin mRNA, complete cds. |
| 53 | CATGAAGAAAGCTC | H32926 | 17 | 4 | 0 | 5 | 1 | R78188 | yi81g01.r1 Homo sapiens cDNA clone 145680 5'. |
| 54 | CATGACACCCATCAC | H70965 | 17 | 4 | 0 | 0 | 0 | M22406 | Human intestinal mucin mRNA, partial cds, clone SM |
| 55 | CATGAGATCCCAAGG | H144707 | 17 | 18 | 0 | 0 | 0 | T24507 | EST082 Homo sapiens cDNA clone 3E6.. |
| | | | | | | | | N79237 | za63a11.s1 Homo sapiens cDNA clone 297212 3' similar to PIR:S49589 S49589 cortical granule lectin - African clawed frog ;. |
| | | | | | | | | T31354 | \EST30893 Homo sapiens cDNA 5' end similar to None.. |
| 56 | CATGAATAGTTTCCC | H52214 | 16 | 4 | 0 | 0 | 0 | H54696 | yq92e02.s1 Homo sapiens cDNA clone 203258 3' simil |
| 57 | CATGCAGAAAGCATC | H295060 | 16 | 9 | 0 | 0 | 0 | M22430 | Human RASF-A PLA2 mRNA, complete cds. |
| 58 | CATGGCTTTGCTTTG | H654976 | 16 | 4 | 2 | 8 | 1 | AA374631 | EST86866 HSC172 cells I Homo sapiens cDNA 5' end |
| | | | | | | | | AA137163 | zn93g08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565790 5' |
| | | | | | | | | AA029320 | zk10f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470145 3' |
| 59 | CATGTGCTGCATTGA | H948543 | 15 | 2 | 0 | 1 | 0 | D25681 | Human colon 3'directed MboI cDNA, HUMGS04047, clon |
| | | | | | | | | AA253331 | zr72g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668978 3' |
| | | | | | | | | H05110 | yl75f07.s1 Homo sapiens cDNA clone 43778 3'. |
| 60 | CATGCCATCGTCCTT | H341720 | 15 | 8 | 1 | 1 | 10 | | Unknown |
| 61 | CATGGAACAGCTCAC | H529013 | 14 | 23 | 0 | 0 | 0 | AA297150 | EST112734 Colon I Homo sapiens cDNA 5' end |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 62 | CATGGGGCTACGTCC | H695406 | 14 | 4 | 0 | 1 | 0 | M25629 | Human kallikrein mRNA, complete cds, clone clone p |
| 63 | CATGCCCGGCTCCTC | H354776 | 14 | 7 | 1 | 5 | 2 | H18836 | ym45d10.s1 Homo sapiens cDNA clone 51262 3'. |
| | | | | | | | | AA026974 | zk01e10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469290 3' |
| | | | | | | | | AA405031 | zu12c12.r1 Soares testis NHT Homo sapiens cDNA clone 731638 5' similar to gb:M61900 Human prostaglandin D synthase gene, complete cds. (HUMAN); |
| 64 | CATGAGGTACTACTA | H176584 | 13 | 9 | 0 | 9 | 8 | U66894 | gb\|U66894\|HSU66894 Human epithelium-restricted Ets protein ESX mRNA, |
| | | | | | | | | U73843 | Human epithelial-specific transcription factor ESE-1b (ESE-1) mRNA, complete cds |
| 65 | CATGCAAATAAATTA | H265232 | 13 | 3 | 0 | 1 | 0 | D25996 | Human colon 3'directed MboI cDNA, HUMGS06772 |
| 66 | CATGCTGTAAAAAAA | H503809 | 13 | 6 | 0 | 1 | 1 | | Unknown |
| 67 | CATGGTTCAATCCCT | H774358 | 13 | 3 | 0 | 2 | 0 | AA071520 | ze88g07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366108 3' |
| | | | | | | | | N90742 | za90h10.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299875 3'. |
| | | | | | | | | AA086292 | zn52h06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 561851 3' |
| 68 | CATGAATAAAGCCTT | H49304 | 12 | 4 | 0 | 0 | 0 | D11499 | Human HepG2 3'-directed MboI cDNA, clone a-35. |
| 69 | CATGGGAAGGTTTAC | H658173 | 12 | 2 | 0 | 1 | 0 | T16031 | IB2474 Homo sapiens cDNA 3'end. |
| 70 | CATGGGATGGCTTAT | H670333 | 12 | 1 | 0 | 6 | 1 | T74426 | yc82e01.r1 Homo sapiens cDNA clone 22306 5'. |
| 71 | CATGGGTGGCCCGGG | H715099 | 12 | 2 | 0 | 3 | 2 | N73771 | za61h02.s1 Homo sapiens cDNA clone 297075 3'. |
| | | | | | | | | W90388 | zh75f08.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417927 3' |
| | | | | | | | | F03786 | H. sapiens partial cDNA sequence; clone c-29h08. |
| 72 | CATGTACTGTACTTC | H817952 | 12 | 2 | 0 | 0 | 0 | U14631 | Human 11 beta-hydroxysteroid dehydrogenase type II |
| 73 | CATGCCCTTGCACTC | H360008 | 11 | 6 | 0 | 3 | 3 | T41121 | ya31a06.s5 Homo sapiens cDNA clone 62194 3' contains Alu repetitive element,. |
| 74 | CATGCGGTGGGACCA | H440966 | 11 | 4 | 0 | 2 | 0 | | Unknown |
| 75 | CATGGCCCCCAACCA | H611590 | 11 | 2 | 0 | 0 | 0 | | Unknown |
| 76 | CATGGCCGGCGCTC | H616862 | 11 | 2 | 0 | 0 | 0 | Z58486 | Unknown |
| 77 | CATGGGAGGCGCTCA | H666014 | 11 | 1 | 0 | 0 | 0 | | Unknown |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 78 | CATGTCCCCGTTACA | H874226 | 11 | 11 | 0 | 0 | 0 | W68073 | zd42c12.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343318 3' similar to contains Alu repetitive element; |

Table 4 - Transcripts increased in pancreas_cancer -

# SAGE Tags elevated only in Pancreatic Tumor

NC Normal Colon
Tu Colon Tumor
CC Colon Cancer Cell Line
PT Pancreatic Tumor
PC Pancreatic Cell Line

| | Tag Sequence | Tag Number | NC | Tu | CC | PT | PC | | Accession | Gene Name |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | CATGAAAGCAAACCA | H9222 | 0 | 6 | 1 | 3 | 11 | Examples | R38305 | yh95b04.s1 Homo sapiens cDNA clone 137455 3' |
| | | | | | | | | | AA126719 | zk95b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490541 3' |
| | | | | | | | | | AA044296 | zk51c03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486340 3' |
| | | | | | | | | | AA131586 | zl33c08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 503726 3' |
| 2 | CATGAAAGCAGTTTA | H9408 | 1 | 5 | 2 | 21 | 3 | Examples | AA157983 | zo71h12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592391 3' |
| | | | | | | | | | AA292929 | zt54e04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726174 3' |
| | | | | | | | | | AA159306 | zo78c07.s1 Stratagene pancreas (#937208) Homo zo78c07.s1 Stratagene pancreas (#937208) Homo |
| | | | | | | | | | R54012 | yj70h01.s1 Homo sapiens cDNA clone 154129 3' |
| | | | | | | | | | T62936 | yb99f08.s1 Homo sapiens cDNA clone 79335 3' |
| 3 | CATGAAAGCGGGGCT | H9898 | 0 | 0 | 0 | 0 | 13 | Examples | X52426 | H. sapiens mRNA for cytokeratin 13 |
| 4 | CATGAAATCCTGGGT | H13803 | 0 | 1 | 1 | 16 | 2 | Examples | X51698 | H.sapiens spasmolytic polypeptide (SP) mRNA. |
| 5 | CATGAAATGGACAAC | H14865 | 0 | 0 | 1 | 0 | 13 | Examples | N70419 | za61d12.s1 Homo sapiens cDNA clone 297047 3' |
| | | | | | | | | | AA411599 | zv16g01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753840 5' |
| | | | | | | | | | AA410508 | zv16g01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753840 3' |
| 6 | CATGAACCAGTTTGT | H21247 | 1 | 1 | 6 | 8 | 13 | Examples | AA115723 | zl86g12.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511558 3' |
| | | | | | | | | | AA132875 | zo19e04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587358 3' |
| | | | | | | | | | AA147677 | zo44a06.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589714 3' |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | AA206883 | zq81h12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 648071 3' |
| 7 | CATGAACTCTTGAAG | H30689 | 3 | 7 | 13 | 13 | 17 | Examples | R51318 | yg72f03.s1 Homo sapiens cDNA clone 38681 3' |
| | | | | | | | | | T35270 | EST82235 Homo sapiens cDNA 3' end similar to None |
| | | | | | | | | | AA412071 | zt65h12.s1 Soares testis NHT Homo sapiens cDNA clone 727271 3' |
| 8 | CATGAACTGCTTCAA | H31221 | 7 | 6 | 8 | 6 | 130 | Examples | N63154 | yz37f12.s1 Homo sapiens cDNA clone 285263 3' |
| | | | | | | | | | T87236 | yc81h04.s1 Homo sapiens cDNA clone 22603 3' |
| | | | | | | | | | AA150720 | zl46f04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 5049 |
| | | | | | | | | | AA045773 | zl68b12.s1 Stratagene colon (#937204) Homo sapiens |
| 9 | CATGAACTTGGCCAT | H32405 | 0 | 0 | 0 | 8 | 11 | Examples | X07819 | Human pump-1 mRNA homolog. to metalloproteinase, |
| | | | | | | | | | L22523 | Human matrilysin gene, exon 5 |
| 10 | CATGAAGATCCCCGC | H36183 | 5 | 10 | 14 | 12 | 23 | Examples | R72650 | yj95e05.s1 Homo sapiens cDNA clone 156512 3' |
| | | | | | | | | | W70287 | zd58e02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344858 3' similar to SW:CUTA_ECOLI P36654 PERIPLASMIC DIVALENT CATION TOLERANCE PROTEIN CUTA |
| | | | | | | | | | R72650 | yj95e05.s1 Homo sapiens cDNA clone 156512 3' similar to SP:CYCY_ECOLI P36654 C-TYPE CYTOCHROME BIOGENESIS PROTEIN CYCY |
| | | | | | | | | | AA181976 | zp61a11.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 624668 3' similar to SW:CUTA_ECOLI P36654 PERIPLASMIC DIVALENT CATION TOLERANCE PROTEIN CUTA |
| 11 | CATGAAGGGAGGGTC | H43180 | 6 | 3 | 8 | 15 | 41 | Examples | U46751 | Human phosphotyrosine independent ligand p62 for tthe Lck SH2 domain mRNA, complete cds |
| 12 | CATGAAGTTGCTATT | H48756 | 10 | 9 | 18 | 31 | 27 | Examples | J03077 | Human co-beta glucosidase (proactivator) mRNA |
| | | | | | | | | | M86181 | Human prosaposin (PSAP) gene |
| | | | | | | | | | D00422 | Human sphingolipid activator proteins, mRNA |
| | | | | | | | | | J03015 | Homo sapiens sphingolipid activator protein 1 mRNA |
| | | | | | | | | | M60255 | Human mutant cerebroside sulfate activator protein |
| 13 | CATGAATGAAAAAAA | H57345 | 0 | 1 | 5 | 2 | 10 | No Match | | |
| 14 | CATGACAAACTGTGG | H66031 | 17 | 4 | 24 | 5 | 60 | Examples | N22375 | yw37d01.s1 Homo sapiens cDNA clone 254401 3' |
| | | | | | | | | | AA084643 | zn20e01.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547992 3' |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | AA279290 | zs84a06.s1 Soares NbHTGBC Homo sapiens cDNA clone 704146 3' | | |
| | | | | | | | | | | | zf12a02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376682 3' | | |
| | | | | | | | | | | AA046253 | | | |
| 15 | CATGACAACTCAATA | H67396 | 2 | 7 | 7 | 16 | 37 | Examples | Z58016 | H.sapiens CpG DNA, clone 26c7. | | | |
| | | | | | | | | | | AA151668 | zo29c02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588290 3' similar to SW:B13_MOUSE P28662 BRAIN PROTEIN 13 | | |
| | | | | | | | | | | | za07e06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone 291874 5' | | |
| | | | | | | | | | | W02958 | | | |
| | | | | | | | | | | | zo70e05.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592256 3' | | |
| 16 | CATGACACCCTGTGC | H71151 | 0 | 1 | 0 | 2 | 14 | Examples | AA1556464 | | ze90h09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366305 3' | | |
| | | | | | | | | | | AA025673 | | | |
| | | | | | | | | | | N70895 | za89h12.s1 Homo sapiens cDNA clone 299783 3' | | |
| 17 | CATGACCATTGGATT | H85924 | 0 | 8 | 5 | 13 | 4 | Examples | X02491 | Human interferon-inducible mRNA (cDNA 9-27): membrane | | | |
| | | | | | | | | | | J04164 | Human interferon-inducible protein 9-27 mRNA | | |
| | | | | | | | | | | X84958 | H.sapiens mRNA for interferon-induced 17kDa membra | | |
| 18 | CATGACCCTTTAACA | H90050 | 1 | 4 | 2 | 13 | 7 | Examples | X56841 | H.sapiens HLA-E gene. | | | |
| | | | | | | | | | | X64879 | H.sapiens mRNA for HLA-E heavy chain (exons 4 - 7) | | |
| 19 | CATGACCGCCGTGGT | H91579 | 49 | 22 | 45 | 70 | 94 | Examples | M21186 | Human neutrophil cytochrome b light chain p22A | | | |
| | | | | | | | | | | M61107 | Human p22-phox (CYBA) gene, exons 3 and 4 | | |
| 20 | CATGACCTGTGACCA | H97158 | 0 | 3 | 0 | 28 | 17 | Examples | D00244 | Human Pro-urokinase gene, | | | |
| | | | | | | | | | | K02286 | Human urokinase gene, 3' end | | |
| | | | | | | | | | | M15476 | Human pro-urokinase mRNA, complete cds | | |
| | | | | | | | | | | X02419 | Human uPA gene for urokinase-plasminogen activator | | |
| 21 | CATGACGCCCTGCTC | H103912 | 0 | 1 | 0 | 11 | 2 | Examples | L08835 | Human myotonic dystrophy kinase (DM kinase) gene | | | |
| | | | | | | | | | | M87313 | Homo sapiens myotonin protein kinase (DM) mRNA | | |
| 22 | CATGACGTGGTGATG | H111380 | 2 | 4 | 4 | 5 | 20 | Examples | H44451 | yo75f06.s1 Homo sapiens cDNA clone 183779 3' | | | |
| | | | | | | | | | | AA157329 | zo42f07.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589573 3' similar to SW:L10K_RAT Q05310 LEYDIG CELL TUMOR 10 KD PROTEIN | | |
| | | | | | | | | | | W46455 | zc32g06.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324058 3' similar to SW:L10K_RAT Q05310 LEYDIG CELL TUMOR 10 KD PROTEIN | | |

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|---|---|---|---|---|---|---|---|---|---|---|
| 23 | CATGACTCAGCCCGG | H119383 | 0 | 0 | 3 | 21 | 3 | Examples | M92357 | Homo sapiens B94 protein mRNA, complete cds. |
| 24 | CATGACTGAGGAAAG | H123521 | 0 | 0 | 0 | 53 | 22 | Examples | X64875 | H.sapiens mRNA for insulin-like growth factor binding protein 3 |
| | | | | | | | | | M31159 | Human growth hormone-dependent insulin-like growth factor binding protein 3 |
| | | | | | | | | | M35878 | Human insulin-like growth factor-binding protein-3 |
| | | | | | | | | | S56205 | insulin-like growth factor binding protein 3 (3' region) |
| 25 | CATGACTGCCCGCTG | H124264 | 1 | 0 | 0 | 22 | 9 | Examples | U65932 | Human extracellular matrix protein 1 (ECM1) mRNA |
| | | | | | | | | | U65937 | Human extracellular matrix protein 1 (ECM1) gene, exon 9 |
| 26 | CATGACTGTATTTTC | H126208 | 3 | 4 | 9 | 2 | 22 | Examples | AA148916 | zo03f09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 566633 3' |
| | | | | | | | | | AA129137 | zo12a11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 586652 3' |
| | | | | | | | | | AA115437 | zl85g09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511456 3' |
| | | | | | | | | | AA126967 | zl87e07.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511620 3' |
| 27 | CATGAGCACTGCAGC | H149395 | 1 | 2 | 6 | 3 | 16 | Examples | R24613 | yh36c03.r1 Homo sapiens cDNA clone 131812 |
| 28 | CATGAGCAGGAGCGT | H150055 | 1 | 0 | 0 | 0 | 15 | Examples | H43243 | yp05e05.r1 Homo sapiens cDNA clone 186560 5' |
| 29 | CATGAGCTGTATTCT | H162622 | 0 | 2 | 0 | 1 | 11 | Examples | X54942 | H.sapiens ckshs2 mRNA for Cks1 protein homologue |
| 30 | CATGAGGATGACCCC | H167446 | 1 | 7 | 12 | 10 | 13 | Examples | AA044081 | zk50g07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486300 3' |
| | | | | | | | | | AA044211 | zk50g07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486300 5' similar to PIR:A40533 A40533 cAMP-dependent protein kinase major membrane substrate |
| 31 | CATGAGGTCTTCAAT | H178129 | 4 | 2 | 0 | 60 | 2 | Examples | X14787 | Class A, Human mRNA for thrombospondin. |
| 32 | CATGAGGTGCGGGGG | H178603 | 0 | 2 | 2 | 1 | 11 | Examples | R27738 | yh64f11.s1 Homo sapiens cDNA clone 134541 3' |
| | | | | | | | | | H00276 | yj22f12.s1 Homo sapiens cDNA clone 149519 3' similar to SP:ZK637.5 CE00436 ARSA |
| 33 | CATGAGTATCTGGGA | H183787 | 3 | 3 | 1 | 15 | 73 | Examples | AA076235 | zm19d07.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526093 3' |
| | | | | | | | | | H13159 | yj16c04.s1 Homo sapiens cDNA clone 148902 3' |
| | | | | | | | | | AA146632 | zo71e11.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592364 3' |
| 34 | CATGATACTTTAATT | H204740 | 1 | 0 | 3 | 18 | 9 | Examples | X80062 | H.sapiens SA mRNA. |
| | | | | | | | | | U01691 | Human annexin V (ANX5) gene |

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|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | X12454 | Human mRNA for vascular anticoagulant |
| | | | | | | | | | M18366 | Human placental anticoagulant protein (PAP) mRNA |
| | | | | | | | | | M21731 | Human lipocortin-V mRNA, complete cds |
| | | | | | | | | | J03745 | Human endonexin II mRNA, complete cds |
| 35 | CATGATCAAGAATCC | H213518 | 2 | 1 | 5 | 25 | 1 | Examples | J03909 | GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR (HUMAN) |
| | | | | | | | | | aa383911 | EST97384 Thymus II Homo sapiens cDNA 3' end similar to interferon, gamma transducer 1 |
| 36 | CATGATCAAGGGTGT | H213679 | 12 | 9 | 25 | 12 | 156 | Examples | U09953 | Human ribosomal protein L9 mRNA |
| | | | | | | | | | U21138 | Human ribosomal protein L9 mRNA, complete cds |
| | | | | | | | | | D14531 | Human mRNA for human homologue of rat ribosomal protein |
| 37 | CATGATCAAGTTCGA | H213751 | 0 | 2 | 8 | 3 | 10 | Examples | AA063259 | zm03a05.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 513008 3' |
| 38 | CATGATCCGGCGCCA | H219750 | 16 | 7 | 14 | 12 | 40 | Examples | L42856 | RNA polymerase II transcription factor SIII p18 subunit mRNA |
| 39 | CATGATGAAACTTCG | H229502 | 1 | 0 | 0 | 17 | 4 | Examples | Z59242 | H.sapiens CpG DNA, clone 13a10, reverse read cpg1 |
| | | | | | | | | | | |
| 40 | CATGATGCGAAAGGC | H235531 | 2 | 3 | 12 | 3 | 22 | Examples | Z25820 | H.sapiens mRNA for mitochondrial dodecenoyl-CoA dehydrogenase |
| | | | | | | | | | L24774 | Homo sapiens delta3, delta2-CoA-isomerase mRNA |
| 41 | CATGATGTCTTCGTT | H243676 | 0 | 0 | 1 | 0 | 14 | Examples | M84711 | 40S RIBOSOMAL PROTEIN S3A (HUMAN) |
| 42 | CATGATGTCTTTTCT | H243710 | 1 | 2 | 1 | 14 | 2 | Examples | M62403 | Human insulin-like growth factor binding protein 4 |
| | | | | | | | | | U20982 | Human insulin-like growth factor binding protein-4 (IGFBP4) gene, promoter and complete cds |
| 43 | CATGATGTGTAACGA | H244487 | 0 | 4 | 5 | 44 | 94 | Examples | Z33457 | H.sapiens mts1 gene. |
| | | | | | | | | | M80563 | Human CAPL protein mRNA, complete cds |
| 44 | CATGCAACTTAAAGC | H270083 | 0 | 1 | 2 | 10 | 1 | Examples | N23207 | yx70b09.s1 Homo sapiens cDNA clone 267065 3' similar to gb:L12350 THROMBOSPONDIN 2 PRECURSOR (HUMAN) |
| 45 | CATGCACCTGTCCTT | H286424 | 0 | 4 | 2 | 10 | 1 | Examples | AA285023 | zt25e11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 714188 3' similar to gb:M33680 CD81 ANTIGEN (HUMAN) |
| | | | | | | | | | M33680 | CD81 antigen |
| 46 | CATGCACTCAATAAA | H291889 | 0 | 0 | 2 | 3 | 19 | Examples | D78203 | Neurosin |
| | | | | | | | | | U62801 | protease M |

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|---|---|---|---|---|---|---|---|---|---|---|
| 47 | CATGCAGCCTGGGGC | H300971 | 0 | 0 | 0 | 0 | 10 | Examples | AA149942 | zo68d04.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592039 3' similar to TR:E218488 E218488 TRYPTASE |
| 48 | CATGCAGCGCGCCCT | H301462 | 4 | 11 | 12 | 10 | 21 | Examples | AA187553 | zp66b09.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 625145 5' similar to gb:M16937 HOMEOBOX PROTEIN HOX-B7 (HUMAN);contains element MER22 repetitive element |
| | | | | | | | | | M16937 | Homeobox protein HOX-B7 |
| 49 | CATGCAGGTTGTCCT | H307126 | 0 | 0 | 4 | 0 | 10 | No Match | | |
| 50 | CATGCAGTCTCTCAA | H309109 | 2 | 6 | 6 | 2 | 17 | Examples | U14972 | Human ribosomal protein S10 mRNA |
| 51 | CATGCATCCCGTGAC | H316857 | 0 | 3 | 3 | 3 | 13 | Examples | U27293 | Human leukotriene A4 hydrolase gene |
| | | | | | | | | | J03459 | Human leukotriene A-4 hydrolase mRNA, complete cds |
| | | | | | | | | | J02959 | Human leukotriene A-4 hydrolase mRNA, complete cds |
| 52 | CATGCATTCCTCCTT | H325080 | 0 | 2 | 5 | 13 | 3 | Examples | X82434 | H.sapiens mRNA for emerin |
| 53 | CATGCCACCCCCACC | H333138 | 3 | 7 | 17 | 18 | 2 | Examples | M88338 | Human serum constituent protein (MSE55) mRNA |
| 54 | CATGCCAGTGGCCCG | H339606 | 23 | 11 | 37 | 22 | 56 | Examples | U14971 | Human ribosomal protein S9 mRNA |
| 55 | CATGCCATTTTCTGG | H344031 | 0 | 2 | 6 | 1 | 10 | Examples | L01697 | Homo sapiens alpha-1 type XV collagen mRNA |
| 56 | CATGCCCAAGCTAGC | H344691 | 19 | 8 | 8 | 18 | 44 | Examples | X54079 | Human mRNA for heat shock protein HSP27. |
| | | | | | | | | | Z23090 | H.sapiens mRNA for 28 kDa heat shock protein |
| | | | | | | | | | X16477 | Human mRNA fragment for estrogen-regulated 24k protein |
| | | | | | | | | | S74571 | estrogen receptor-related protein=27-kda heat shock protein |
| 57 | CATGCCCATCCGAAA | H347489 | 20 | 15 | 43 | 19 | 61 | Examples | X69392 | H.sapiens mRNA for ribosomal protein L26. |
| | | | | | | | | | L07287 | Human ribosomal protein L26 (RPL26) gene |
| 58 | CATGCCCCCTGCAGA | H350099 | 0 | 1 | 6 | 14 | 25 | Examples | U40434 | Human mesothelin or CAK1 antigen precursor mRNA |
| | | | | | | | | | D49441 | Human mRNA for pre-pro-megakaryocyte potentiating factor, complete cds. |
| 59 | CATGCCCGCATAGAT | H353481 | 0 | 0 | 0 | 8 | 11 | Examples | U12819 | Human p16-INK4 (p16) gene |
| | | | | | | | | | U38945 | Human hypothetical 18.1 kDa protein (CDKN2A) mRNA |
| | | | | | | | | | S69804 | MTS1=multiple tumor suppressor 1/cyclin-dependent kinase 4 inhibitor p16 |
| | | | | | | | | | S69822 | CDK4I=cyclin-dependent kinase 4 inhibitor |
| | | | | | | | | | S78535 | tumor suppressor gene, P16/MTS1/CDKN2=cell cycle cycle negative regulator beta form |
| 60 | CATGCCCTCCTGGGG | H357867 | 8 | 2 | 5 | 14 | 34 | Examples | Z47319 | H.sapiens mRNA for expressed sequence tag (clone 21fi7119) |

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|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | AA398406 | zt60h12.s1 Soares testis NHT Homo sapiens cDNA clone 726791 3' |
| 61 | CATGCCGGCCCTACC | H370034 | 4 | 4 | 1 | 14 | 19 | Examples | U21049 | Human DD96 mRNA |
| 62 | CATGCCTGGTCCCAA | H387925 | 0 | 2 | 1 | 30 | 99 | Examples | X03212 | KERATIN, TYPE II CYTOSKELETAL 7 |
| | | | | | | | | | AA187637 | zp73f01.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 625849 3' |
| 63 | CATGCCTTTGAACAG | H392709 | 5 | 3 | 6 | 2 | 23 | Examples | AA176457 | zp35g11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 611492 3' similar to TR:G663269 G663269 BOLA |
| | | | | | | | | | AA176541 | zp35e11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 611468 3' similar to TR:G663269 G663269 BOLA. |
| 64 | CATGCGCCGACGATG | H415844 | 21 | 13 | 45 | 75 | 7 | Examples | X02492 | Human interferon-inducible mRNA fragment |
| 65 | CATGCTCAACAGCAA | H475429 | 2 | 5 | 10 | 6 | 17 | Examples | T53402 | ya88g05.s1 Homo sapiens cDNA clone 68792 3' |
| | | | | | | | | | W69493 | zd47g08.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343838 3' similar to PIR:S24168 S24168 hypothetical protein - human |
| 66 | CATGCTCAACCCCCC | H475478 | 1 | 4 | 2 | 23 | 1 | Examples | X13916 | Human mRNA for LDL-receptor related protein |
| 67 | CATGCTGAGAAACTG | H493576 | 2 | 3 | 1 | 8 | 18 | Examples | X80335 | H.sapiens (24) Ferritin H pseudogene. |
| 68 | CATGCTGAGTCTCCC | H494454 | 1 | 4 | 4 | 21 | 13 | Examples | X04828 | Human mRNA for G(i) protein alpha-subunit |
| 69 | CATGCTGCTATACGA | H498887 | 16 | 30 | 28 | 30 | 44 | Examples | U14966 | Human ribosomal protein L5 mRNA |
| 70 | CATGCTGCTGAGTGA | H499247 | 1 | 3 | 4 | 13 | 13 | Examples | T90665 | yd41g08.s1 Homo sapiens cDNA clone 110846 3' |
| | | | | | | | | | AA338799 | EST43791 Fetal brain I Homo sapiens cDNA 3' end similar to steroid hormone receptor hERR1 |
| | | | | | | | | | H97236 | yv98b06.s1 Homo sapiens cDNA clone 250739 3' |
| 71 | CATGCTGGCGCCGAT | H501337 | 0 | 0 | 4 | 0 | 10 | Examples | C14084 | Human fetal brain cDNA 3'-end GEN-018D10 |
| 72 | CATGCTTCCAGCTAA | H513181 | 64 | 23 | 36 | 53 | 104 | Examples | D00017 | Human lipocortin II mRNA |
| 73 | CATGCTTCCTTGCCT | H514022 | 0 | 3 | 4 | 89 | 7 | Examples | Z19574 | H.sapiens gene for cytokeratin 17. |
| | | | | | | | | | X62571 | H.sapiens mRNA for keratin-related protein |
| | | | | | | | | | X05803 | Human radiated keratinocyte mRNA 266 |
| 74 | CATGCTTTCTTCCCT | H522198 | 0 | 2 | 1 | 16 | 4 | Examples | X79067 | H.sapiens ERF-1 mRNA 3' end. |
| 75 | CATGGAAAAAAAAAA | H524289 | 7 | 14 | 21 | 26 | 37 | Examples | X51779 | Human mRNA containing an Alu repeat |
| | | | | | | | | | X82240 | H.sapiens mRNA for Tcell leukemia/lymphoma 1 |
| 76 | CATGGAAACAAGATG | H525348 | 4 | 7 | 14 | 8 | 22 | Examples | V00572 | Human mRNA encoding phosphoglycerate kinase. |
| | | | | | | | | | D29018 | Human keratinocyte cDNA, clone 001 |
| | | | | | | | | | L00160 | Human phosphoglycerate kinase (pgk) mRNA |
| 77 | CATGGAAATACAGTT | H527436 | 49 | 35 | 10 | 100 | 36 | Examples | X05344 | Human mRNA for cathepsin D |

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|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | M11233 | Human cathepsin D mRNA, complete cds |
| 'S | CATGGAAATGATGAG | H527929 | 4 | 7 | 5 | 14 | 26 | Examples | T90296 | yd42f03.s1 Homo sapiens cDNA clone 110909 3' similar to SP:R151.9 CE00827 |
| | | | | | | | | | AA320942 | EST23523 Adipose tissue, brown Homo sapiens cDNA 3' end |
| '9 | CATGGAAGATGTGTG | H513436 | 3 | 7 | 16 | 6 | 28 | Examples | AA181811 | zp64f07.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 624997 3' |
| | | | | | | | | | AA148508 | zl06c06 s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491530 3' similar to WP:ZK652.2 CE00448 |
| 80 | CATGGAATTTTATAA | H540621 | 6 | 3 | 10 | 9 | 28 | Examples | L21950 | Human peripheral benzodiazepine receptor related mRNA |
| | | | | | | | | | M36035 | Human peripheral benzodiazepine receptor (hpbs) mRNA |
| 81 | CATGGACAAAAAAAA | H540673 | 1 | 2 | 10 | 3 | 17 | No Match | | |
| 82 | CATGGACCACCTTTA | H545152 | 0 | 1 | 0 | 11 | 2 | Examples | U19718 | Human microfibril-associated glycoprotein (MFAP2). |
| 83 | CATGGACCAGGCCCT | H545430 | 0 | 3 | 0 | 20 | 18 | Examples | M75165 | H.sapiens epithelial tropomyosin (TM1) mRNA |
| | | | | | | | | | M12125 | Human fibroblast muscle-type tropomyosin mRNA |
| | | | | | | | | | M74817 | Human tropomyosin-1 (TM-beta) mRNA, complete cds |
| 84 | CATGGACCCCAAGGC | H546059 | 2 | 5 | 9 | 16 | 10 | Examples | M74092 | Human cyclin mRNA |
| 85 | CATGGACCCTGCCCT | H546710 | 31 | 36 | 20 | 71 | 65 | Examples | L37033 | Homo sapiens FK-506 binding protein homologue |
| 86 | CATGGACCTATCTCT | H548062 | 0 | 1 | 0 | 13 | 1 | Examples | N90046 | zb37g02.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305810 3' |
| | | | | | | | | | AA115048 | zl06a10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491514 3' |
| 87 | CATGGACGGCGCAGG | H551315 | 3 | 4 | 5 | 32 | 3 | Examples | M63193 | Human platelet-derived endothelial cell growth factor |
| 88 | CATGGACTCTCTGTT | H554876 | 1 | 4 | 3 | 0 | 14 | Examples | M61764 | Human gamma-tubulin mRNA, |
| 89 | CATGGAGAGCTTTGC | H559615 | 0 | 0 | 0 | 2 | 10 | Examples | D17793 | Human mRNA (HA1753) for ORF |
| 90 | CATGGAGAGTGTCTG | H560056 | 0 | 5 | 8 | 32 | 11 | Examples | S68252 | TIMP-1=metalloproteinase inhibitor |
| | | | | | | | | | X02598 | EPA glycoprotein (erythroid-potentiating activity) |
| | | | | | | | | | X03124 | tissue inhibitor of metalloproteinase 2 |
| 91 | CATGGAGCAGGATGA | H561807 | 0 | 0 | 0 | 1 | 12 | No Match | | |
| 92 | CATGGAGGGAGTTCC | H567486 | 1 | 1 | 0 | 4 | 13 | Examples | AA214523 | zr89c01.s1 Soares NbHTGBC Homo sapiens cDNA clone 682848 3' |
| | | | | | | | | | N30324 | yw75d01.s1 Homo sapiens cDNA clone 258049 3' |
| 93 | CATGGAGTCCGGAGC | H570787 | 0 | 0 | 2 | 1 | 10 | Examples | X70070 | H.sapiens mRNA for neurotensin receptor. |
| 94 | CATGGAGTTATGTTG | H572656 | 0 | 0 | 3 | 0 | 10 | Examples | H57673 | yr27a10.s1 Homo sapiens cDNA clone 206490 3' |

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|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | W94333 | ze12c08.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358766 3' similar to SW:YA94_SCHPO Q09783 HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I |
| 95 | CATGGAGTTCGACCT | H572806 | 7 | 3 | 7 | 15 | 29 | No Match | | |
| 96 | CATGGATTAAGTGAG | H585913 | 3 | 5 | 2 | 2 | 19 | Examples | AA046631 | zk72d06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488363 3' |
| | | | | | | | | | R91942 | yq06g03.s1 Homo sapiens cDNA clone 196180 3' |
| | | | | | | | | | AA040439 | zk46c12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485878 3' |
| 97 | CATGGATTGAACCTC | H587800 | 1 | 0 | 5 | 1 | 12 | Examples | U60205 | methyl sterol oxidase (ERG25) |
| 98 | CATGGCAAAAAAAAA | H589825 | 17 | 13 | 29 | 73 | 38 | No Match | | |
| 99 | CATGGCATTTAAATA | H605956 | 2 | 10 | 8 | 3 | 55 | Examples | X60489 | Human mRNA for elongation factor-1-beta. |
| | | | | | | | | | X60656 | H.sapiens mRNA for elongation factor 1-beta |
| 100 | CATGGCCAACAACGA | H606471 | 0 | 0 | 0 | 12 | 1 | Examples | U08021 | Human nicotinamide N-methyltransferase (NNMT) mRNA, 0 |
| 101 | CATGGCCCCCAATAA | H611597 | 1 | 4 | 1 | 47 | 9 | Examples | X15256 | Human mRNA for 14kDa beta-galactoside-binding lectin |
| | | | | | | | | | X14829 | Human mRNA for beta-galactoside-binding lectin |
| | | | | | | | | | J04456 | Human 14 kd lectin mRNA, complete cds |
| | | | | | | | | | S44881 | HL14=beta-galactoside binding protein |
| 102 | CATGGCCGCTACTTC | H616224 | 0 | 0 | 1 | 3 | 16 | Examples | AA054483 | zk82d04.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489319 5' similar to contains Alu repetitive element |
| 103 | CATGGCCGTCGGAGG | H617891 | 8 | 5 | 2 | 44 | 3 | Examples | AA243725 | zr68g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668614 3' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16 PRECURSOR (HUMAN) |
| 104 | CATGGCCTACCCGAG | H618841 | 0 | 4 | 4 | 23 | 39 | Examples | X13425 | Human mRNA for pancreatic carcinoma marker GA733-1, 0 |
| 105 | CATGGCGGGGTGGAG | H633577 | 3 | 8 | 5 | 27 | 6 | Examples | AA136985 | zl02b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491117 3' |
| 106 | CATGGCTCAGCTGGA | H643707 | 12 | 29 | 24 | 35 | 35 | Examples | AA053346 | zl70h04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510007 3' similar to gb:Z21507 ELONGATION FACTOR 1-DELTA |
| 107 | CATGGCTTTTCAGAC | H655177 | 1 | 6 | 7 | 13 | 10 | Examples | U43368 | Human VEGF related factor isoform VRF186 precursor, 0 |
| | | | | | | | | | U52819 | Human vascular endothelial growth factor B 186 |
| 108 | CATGGGAAAAAAAAA | H655361 | 11 | 8 | 30 | 16 | 38 | Examples | M38259 | Human cytochrome c oxidase subunit VIb |
| | | | | | | | | | M60748 | Human histone H1 (H1F4) gene, complete cds |

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|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | M73239 | Human (clone SF1) hepatocyte growth factor (HGF) |
| | | | | | | | | | M73240 | Human (clone SF2) hepatacyte growth factor (HGF) |
| 109 | CATGGGAAAAGTGGT | H655547 | 18 | 13 | 3 | 70 | 1 | Examples | X02920 | Human mRNA for alpha 1-antitrypsin carboxyterminal, 0 |
| | | | | | | | | | X01683 | Human mRNA for alpha 1-antitrypsin |
| | | | | | | | | | V00496 | Human messenger RNA for alpha-1-antitrypsin |
| | | | | | | | | | J00067 | Human alpha-1 antitrypsin gene, 3' end |
| 110 | CATGGGAAGGGAGGC | H658059 | 0 | 0 | 4 | 6 | 16 | Examples | AA127040 | zl22b01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502633 3' |
| | | | | | | | | | W81387 | zd86f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347555 3' |
| | | | | | | | | | H45477 | yo72h08.s1 Homo sapiens cDNA clone 183519 3' |
| 111 | CATGGGAGTCATTGT | H666943 | 6 | 5 | 6 | 10 | 32 | Examples | D26598 | Human mRNA for proteasome subunit HsC10-II. , 0 |
| 112 | CATGGGAGTGTGCGT | H667367 | 0 | 0 | 1 | 1 | 10 | Examples | N74310 | za78c01.s1 Homo sapiens cDNA clone 298656 3' |
| | | | | | | | | | H92750 | yt92e01.s1 Homo sapiens cDNA clone 231768 3' |
| | | | | | | | | | T24084 | seq2272 Homo sapiens cDNA clone ssb4HB3MA(extended-ft-6) 3' |
| 113 | CATGGGATTGTCTGG | H671455 | 3 | 7 | 13 | 5 | 21 | Examples | X17567 | H.sapiens RNA for snRNP protein B |
| | | | | | | | | | M34081 | Human small nuclear ribonucleoprotein particle SmB |
| 114 | CATGGGCCCCTCACC | H677330 | 0 | 0 | 2 | 9 | 22 | Examples | M69054 | Human insulin-like growth factor binding protein 6, 0 |
| | | | | | | | | | M62402 | Human insulin-like growth factor binding protein 6 |
| 115 | CATGGGCCCTCTGAG | H677753 | 0 | 1 | 4 | 7 | 14 | Examples | N74323 | za78d08.s1 Homo sapiens cDNA clone 298671 3' |
| | | | | | | | | | H46766 | yo18f08.s1 Homo sapiens cDNA clone 178311 3' |
| | | | | | | | | | H41102 | yn88a08.s1 Homo sapiens cDNA clone 175478 3' |
| 116 | CATGGGCTGGTCTGG | H686815 | 0 | 1 | 3 | 13 | 22 | Examples | AA074777 | zm84b09.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544601 3' |
| | | | | | | | | | AA062735 | zm04a04.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 513102 3' |
| | | | | | | | | | AA112905 | zm63f12.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone 530351 3' |
| 117 | CATGGGGAAGCAGAT | H688713 | 25 | 7 | 9 | 0 | 72 | No Match | | |
| 118 | CATGGGGAGGGGTGG | H690863 | 2 | 3 | 1 | 16 | 2 | No Match | | |
| 119 | CATGGGGAGGTAGCA | H690890 | 1 | 0 | 1 | 14 | 1 | No Match | | |
| 120 | CATGGGGCATCTCTT | H693112 | 1 | 1 | 3 | 39 | 2 | Examples | V00523 | Human mRNA for histocompatibility antigen HLA-DR |
| | | | | | | | | | X00274 | Human gene for HLA-DR alpha heavy chain a class II |
| | | | | | | | | | K01171 | Human HLA-DR alpha-chain mRNA |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | J00202 | human hla-dr heavy chain gene; 3' flank |
| 121 | CATGGGTGGGGAGAT | H715401 | 1 | 4 | 10 | 10 | 14 | Examples | U18009 | Human chromosome 17q21 mRNA clone LF113. |
| | | | | | | | | | T33413 | EST57778 Homo sapiens cDNA 3' end similar to None |
| | | | | | | | | | T33339 | EST57474 Homo sapiens cDNA 3' end similar to None |
| 122 | CATGGTACTGTAGCA | H728778 | 3 | 3 | 1 | 16 | 30 | Examples | M59911 | Human integrin alpha-3 chain mRNA |
| 123 | CATGGTACTGTGGCT | H728810 | 23 | 10 | 16 | 15 | 50 | Examples | X87689 | H.sapiens mRNA for putative p64 CLCP protein |
| 124 | CATGGTCAAAATTTC | H737344 | 0 | 0 | 0 | 10 | 1 | Examples | L12350 | Human thrombospondin 2 (THBS2) mRNA |
| 125 | CATGGTCTGGGGCTT | H752296 | 25 | 35 | 45 | 76 | 29 | Examples | D21261 | Human mRNA (HA1756) for ORF |
| | | | | | | | | | D29543 | Human keratinocyte cDNA, clone 686 |
| 126 | CATGGTCTGTGAGAG | H752521 | 0 | 5 | 7 | 12 | 2 | Examples | H51290 | yp07a05.s1 Homo sapiens cDNA clone 186704 3' |
| | | | | | | | | | N20338 | yx44g12.s1 Homo sapiens cDNA clone 264646 3' |
| | | | | | | | | | AA158271 | zo76e09.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 592840 3' |
| 127 | CATGGTCTGTGCAGG | H752531 | 0 | 0 | 0 | 1 | 13 | No Match | | |
| 128 | CATGGTCTTGAAGCC | H753162 | 0 | 1 | 2 | 1 | 10 | No Match | | |
| 129 | CATGGTGAAGGCAGT | H754323 | 25 | 14 | 42 | 15 | 89 | Examples | X87373 | Class C, H.sapiens RPS3a gene |
| 130 | CATGGTGAATGACGG | H754567 | 0 | 2 | 8 | 1 | 10 | Examples | X08058 | GLUTATHIONE S-TRANSFERASE P (HUMAN) |
| 131 | CATGGTGCGGAGGAC | H760361 | 0 | 3 | 2 | 11 | 25 | Examples | X51439 | Human mRNA for serum amyloid A (SAA) protein |
| 132 | CATGGTGCTGGAGAA | H761481 | 2 | 9 | 9 | 13 | 26 | Examples | U15008 | Human SnRNP core protein Sm D2 mRNA |
| 133 | CATGGTGGAGGGCAC | H762533 | 1 | 1 | 3 | 6 | 34 | Examples | U62800 | Cystatin M (CST6) |
| 134 | CATGGTGGTACAGGA | H765003 | 14 | 17 | 15 | 39 | 30 | Examples | H46430 | yo12h12.s1 Homo sapiens cDNA clone 177767 3' |
| | | | | | | | | | AA047563 | zf13a06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376786 3' |
| | | | | | | | | | AA130701 | zo13f02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 586779 3' |
| 135 | CATGGTTCACTGCAG | H774629 | 0 | 2 | 1 | 13 | 3 | Examples | X59288 | H.sapiens gene for intercellular adhesion molecule |
| | | | | | | | | | M24283 | Human major group rhinovirus receptor (HRV) mRNA |
| | | | | | | | | | J03132 | Human intercellular adhesion molecule-1 (ICAM-1) |
| | | | | | | | | | M55100 | Human cell surface glycoprotein P3.58 mRNA |
| 136 | CATGGTTGTCTTTGG | H781823 | 1 | 1 | 6 | 30 | 24 | Examples | K02765 | Human complement component C3 mRNA, alpha and beta |
| 137 | CATGGTTGTGGTTAA | H782013 | 178 | 110 | 14 | 340 | 139 | Examples | M17987 | Human beta-2-microglobulin gene |
| 138 | CATGGTTTAAATCGA | H782391 | 1 | 6 | 12 | 4 | 14 | Examples | D00760 | Human mRNA for proteasome subunit HC3 |
| 139 | CATGTAAGGCTTAAC | H797169 | 0 | 0 | 6 | 1 | 12 | Examples | X57025 | INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN) |
| 140 | CATGTAATTTTGGAA | H802793 | 0 | 2 | 5 | 2 | 10 | No Match | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | CATGTAATTTTGGAT | H802793 | | | | | No Match | | | |
| 11 | CATGTACATTTTCAT | H806901 | 1 | 4 | 2 | 3 | 14 | Examples | X85373 | H.sapiens mRNA for Sm protein G |
| 12 | CATGTACCCCGTACA | H808370 | 0 | 1 | 4 | 0 | 10 | No Match | | |
| 13 | CATGTACCCTTCTAT | H808925 | 0 | 0 | 0 | 17 | 7 | No Match | | |
| 14 | CATGTAGGAAAGTAA | H827437 | 1 | 0 | 5 | 5 | 24 | Examples | J02931 | Human placental tissue factor (two forms) mRNA |
| | | | | | | | | | M16553 | Human tissue factor mRNA, complete cds |
| | | | | | | | | | M27436 | Human tissue factor gene, complete cds |
| 15 | CATGTAGGTTGTCTA | H831416 | 49 | 61 | 61 | 89 | 130 | Examples | X64899 | H.sapiens mRNA homologous to mouse P21 mRNA. |
| | | | | | | | | | X16064 | Human mRNA for translationally controlled tumor protein |
| | | | | | | | | | L13806 | Homo sapiens (clone 04) translationally controlled tumor protein |
| 16 | CATGTATATTTTCTC | H839672 | 1 | 0 | 3 | 8 | 16 | Examples | M98479 | Human transglutaminase mRNA |
| 17 | CATGTATTTTCTGCC | H851834 | 0 | 1 | 2 | 16 | 3 | Examples | D12149 | Human HepG2 3'-directed MboI cDNA, clone s247 |
| 18 | CATGTCACAAGCAAA | H856209 | 10 | 28 | 27 | 24 | 48 | Examples | X80909 | H.sapiens alpha NAC mRNA |
| 19 | CATGTCCAAATCGAT | H868569 | 0 | 1 | 0 | 43 | 17 | Examples | X56134 | Human mRNA for vimentin. |
| | | | | | | | | | Z19554 | H.sapiens vimentin gene |
| | | | | | | | | | M14144 | Human vimentin gene, complete cds |
| | | | | | | | | | M25246 | Human vimentin (HuVim3) mRNA, 3' end |
| 20 | CATGTCCACTGGCCT | H870310 | 0 | 0 | 1 | 12 | 2 | Examples | N92906 | zb57a08.s1 Homo sapiens cDNA clone 307670 3' |
| | | | | | | | | | T17488 | NIB978 Normalized infant brain, Bento Soares Homo sapiens cDNA 3'end |
| | | | | | | | | | AA349906 | EST56900 Infant brain Homo sapiens cDNA 3' end |
| 151 | CATGTCCATCTGTTG | H871920 | 6 | 6 | 10 | 25 | 5 | Examples | X67016 | H.sapiens mRNA for amphiglycan |
| | | | | | | | | | D13292 | Human mRNA for ryudocan core protein |
| 152 | CATGTCGTCTTTATC | H899060 | 2 | 5 | 15 | 1 | 69 | Examples | M77233 | Human ribosomal protein S7 mRNA |
| 153 | CATGTCTCTGATGCT | H908858 | 1 | 5 | 2 | 46 | 19 | Examples | S48568 | tissue inhibitor of metalloproteinase 2 (3'-end region) |
| | | | | | | | | | | |
| | | | | | | | | | | |
| 154 | CATGTCTTGTAACTG | H916232 | 0 | 4 | 3 | 1 | 13 | Examples | N71680 | yz93b03.s1 Homo sapiens cDNA clone 290573 3' |
| 155 | CATGTCTTGTGCATA | H916372 | 14 | 22 | 15 | 20 | 45 | Examples | X03083 | Human lactate dehydrogenase-A gene |
| | | | | | | | | | X02152 | Human mRNA for lactate dehydrogenase-A |
| | | | | | | | | | X02153 | Human pseudogene for lactate dehydrogenase-A |
| 156 | CATGTGAAGTCACTG | H920392 | 1 | 1 | 6 | 0 | 16 | No Match | | |
| 157 | CATGTGAAGTTATAC | H920525 | 0 | 1 | 3 | 6 | 11 | Examples | X07979 | CTGTGG, Class A, Human mRNA for fibronectin receptor beta subunit. |

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|---|---|---|---|---|---|---|---|---|---|---|
| 158 | CATGTGATGTCTGGT | H932731 | 0 | 8 | 3 | 11 | 12 | Examples | AA027860 | zk05h07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469693 3' |
| 159 | CATGTGCCATCTGTA | H938876 | 1 | 3 | 7 | 3 | 16 | Examples | M25753 | G2/MITOTIC-SPECIFIC CYCLIN B1 (HUMAN) |
| | | | | | | | | | T60151 | yc22c04.s1 Homo sapiens cDNA clone 81414 3' |
| | | | | | | | | | R67969 | yi29g08.s1 Homo sapiens cDNA clone 140702 3' |
| 160 | CATGTGCCCTCAAAA | H939841 | 11 | 13 | 3 | 13 | 43 | Examples | AA169614 | zo91f03.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594269 3' similar to SW:NGAL_HUMAN P80188 NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR |
| 161 | CATGTGCCCTCAGAA | H939849 | 3 | 4 | 0 | 11 | 19 | Examples | N79823 | zb15d08.s1 Homo sapiens cDNA clone 302127 3' similar to SW:NGAL_HUMAN P80188 NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR |
| 162 | CATGTGCCCTCAGGA | H939851 | 13 | 31 | 10 | 25 | 83 | Examples | AA075896 | zm90h04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545239 3' similar to SW:NGAL_HUMAN P80188 NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR |
| 162 | CATGTGCCCTCAGGC | H920392 | | | | | | No Match | | |
| 163 | CATGTGCCTTACTTT | H941856 | 0 | 3 | 1 | 2 | 12 | Examples | AA100279 | zl81e07.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511044 3' |
| 164 | CATGTGCGCTGGCCC | H944038 | 2 | 5 | 2 | 17 | 3 | No Match | | |
| 165 | CATGTGCTTCATCTG | H949560 | 2 | 6 | 6 | 4 | 16 | Examples | AA029262 | zk10a01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470088 3' |
| | | | | | | | | | N54281 | yv66e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 247722 3' |
| | | | | | | | | | AA114075 | zn76c02.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 564098 3' |
| 166 | CATGTGGAGTGGAGG | H953251 | 18 | 15 | 7 | 22 | 48 | Examples | L76200 | Homo sapiens guanylate kinase (GUK1) mRNA |
| 167 | CATGTGGCCCCAGGT | H955723 | 0 | 3 | 3 | 37 | 4 | Examples | X00570 | Human mRNA for precursor of apolipoprotein CI |
| 168 | CATGTGGGTGAGCCA | H962086 | 13 | 15 | 13 | 76 | 27 | Examples | L16510 | Homo sapiens cathepsin B mRNA |
| | | | | | | | | | M14221 | Human cathepsin B proteinase mRNA, complete cds |
| 169 | CATGTGTGAGCCCCT | H975446 | 3 | 3 | 3 | 22 | 8 | Examples | L35240 | Human enigma gene |
| 170 | CATGTGTGCTAAATG | H976644 | 8 | 21 | 26 | 18 | 50 | Examples | L38941 | Homo sapiens ribosomal protein L34 (RPL34) mRNA |
| 171 | CATGTGTGTGTTTGT | H978687 | 6 | 7 | 16 | 25 | 15 | Examples | X03473 | Human gene for histone H1(0). |
| 172 | CATGTTATGGATCTC | H997944 | 0 | 1 | 1 | 21 | 1 | Examples | AA034505 | zk23g08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471422 3' |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | AA235464 | | | zt31b06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 723923 3' |
| | | | | | | | | | AA037024 | | | 2k30c10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 472050 3' |
| CATGTTCATTGTAGA | H1003443 | 0 | 7 | 0 | 10 | 3 | Examples | H53629 | | | | yu38d04.s1 Homo sapiens cDNA clone 236071 3' |
| | | | | | | | | T06706 | | | | EST04595 Homo sapiens cDNA clone HFBDX32 |
| | | | | | | | | T16635 | | | | NIB1599 Normalized infant brain, Bento Soares Homo sapiens cDNA 3'end similar to EST04595 H. sapiens cDNA clone HFBDX32 |
| CATGTTCTGTGAATC | H1014660 | 3 | 4 | 3 | 24 | 5 | Examples | AA026678 | | | | ze97h02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366963 3' |
| | | | | | | | | | AA280283 | | | zt05a03.s1 Soares NbHTGBC Homo sapiens cDNA clone 712204 3' |
| | | | | | | | | | H10141 | | | ym05a09.s1 Homo sapiens cDNA clone 46675 3' |
| CATGTTGCCCCCGTG | H1021276 | 0 | 0 | 0 | 8 | 17 | Examples | X66029 | | | | H.sapiens mRNA for tyrosine kinase receptor. |
| CATGTTGCTGACTTT | H1023520 | 1 | 5 | 1 | 33 | 1 | Examples | X15880 | | | | Human mRNA for collagen VI alpha-1 |
| | | | | | | | | X72414 | | | | H.sapiens gene for glutaminyl-tRNA synthetase |
| CATGTTGGAGATCTC | H1024568 | 4 | 11 | 16 | 10 | 24 | Examples | AA044568 | | | | zk73h10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488515 3' |
| | | | | | | | | N71899 | | | | yz36b07.s1 Homo sapiens cDNA clone 285109 3' |
| | | | | | | | | | AA400793 | | | zt71g03.s1 Soares testis NHT Homo sapiens cDNA clone 727828 3' |
| CATGTTGGGGTTTCC | H1026814 | 202 | 75 | 84 | 235 | 369 | Examples | X80336 | | | | H.sapiens (5) Ferritin H pseudogene. |
| | | | | | | | | X00318 | | | | Human mRNA for apoferritin H chain type |
| | | | | | | | | X03488 | | | | Human apoferritin H gene exons 2-4 |
| | | | | | | | | M97164 | | | | Human ferritin heavy chain mRNA, complete cds |
| | | | | | | | | L20941 | | | | Human ferritin heavy chain mRNA, complete cds |
| CATGTTGGTGAAGGA | H1027595 | 98 | 106 | 17 | 183 | 107 | Examples | X02493 | | | | Human interferon-inducible mRNA (cDNA 6-26). |
| | | | | | | | | M11948 | | | | Human promyelocytic leukemia cell mRNA |
| | | | | | | | | M17733 | | | | Human thymosin beta-4 mRNA, complete cds |
| CATGTTTCCCTCAAA | H1037777 | 0 | 1 | 0 | 13 | 1 | Examples | N78832 | | | | zb17a08.s1 Homo sapiens cDNA clone 302294 3' |
| | | | | | | | | | AA411095 | | | zt33d02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 724131 3' |
| | | | | | | | | W81693 | | | | zd84g11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347396 3' |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| SI | CATGTTTCCTTCCTT | H1038296 | 0 | 6 | 3 | 7 | 17 | Examples | M20471 | Human brain-type clathrin light-chain a mRNA |
| | | | | | | | | | M20472 | Human lymphocyte clathrin light-chain A mRNA |
| IS2 | CATGTTTGCACCTTT | H1041504 | 2 | 0 | 0 | 16 | 1 | Examples | X78947 | H.sapiens mRNA for connective tissue growth factor |
| | | | | | | | | | U14750 | Human connective tissue growth factor mRNA |
| IS4 | CATGTTTGTTAAAA | H1044225 | | | | | | | H06492 | yi78c08.s1 Homo sapiens cDNA clone 44273 3' |
| | | | | | | | | | T35952 | EST94173 Homo sapiens cDNA 3' end similar to None |
| | | | | | | | | | AA253218 | zr53g10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667170 3' |

Table 5 - Transcripts increased in pancreas and colorectal cancer

SAGE tag that were elevated in both in coloreactal and pancreatic tumor, and are likely to be specific for tumor in general.

| | Tag_Sequence | Tag_Number | Accession | Description |
|---|---|---|---|---|
| 1 | CATG TGGAAATGAC C | -950498 | M10629 | Human alpha-1 collagen gene, 3' end with polyA sit |
| 2 | CATG CACTTCAAGG G | -294155 | U42376 | Human retinoic acid induced RIG-E precursor (E) mR |
| | | | U56145 | Human thymic shared antigen-1/stem cell antigen-2 |
| 3 | CATG ATGTGAAGAG T(A) | -243747 | J03040 | Human SPARC/osteonectin mRNA, complete cds. |
| | | | M25746 | Human osteonectin gene exon 10, complete cds. |
| 4 | CATG GCCCAAGGAC C | -610466 | X53416 | Human mRNA for actin-binding protein (filamin) (AB |
| 5 | CATG ATCTTGTTAC T | -229106 | X02761 | Human mRNA for fibronectin (FN precursor). |
| | | | K00799 | human fibronectin (fn) 3' coding region and flank, |
| 6 | CATG GTGCGCTGAG C | -760291 | X58536 | Human mRNA for HLA class I locus C heavy chain. |
| | | | M26432 | Human MHC class I HLA-C.1 gene, complete cds. |
| 7 | CATG ACAGGCTACG G | -76231 | M95787 | Human 22kDa smooth muscle protein (SM22) mRNA, com |
| | | | M83106 | Human SM22 mRNA, 5' end. |
| 8 | CATG GTGTGTTTGT A | -769020 | M77349 | Human transforming growth factor-beta induced gene |
| 9 | CATG GATTTCTCAG C | -589267 | X53279 | Human mRNA for placental-like alkaline phosphatase |
| | | | X55958 | H.sapiens mRNA for alkaline phosphatase. |
| | | | J04948 | Human alkaline phosphatase (ALP-1) mRNA, complete |
| 10 | CATG ACCATTCTGC T | -85882 | X57351 | Human 1-8D gene from interferon-inducible gene fam |
| | | | X02490 | Human interferon-inducible mRNA (cDNA 1-8). |
| 11 | CATG TCCTTCTCCA C | -884181 | X15804 | Human mRNA for alpha-actinin. |
| 12 | CATG CTTCTGTGTA C,T | -515821 | D80012 | Human mRNA for KIAA0190 protein. |
| 13 | CATG ATGTAAAAAA T | -241665 | M74090 | Human TB2 gene mRNA, 3' end. |
| | | | J03801 | Human lysozyme mRNA, complete cds with an Alu repe |
| | | | M19045 | Human lysozyme mRNA, complete cds. |
| 14 | CATG GGCAGAGGAC C | -673954 | X17620 | Human mRNA for Nm23 protein, involved in developme |
| | | | X75598 | H.sapiens nm23H1 gene. |
| 15 | CATG AATATTGAGA A | -53129 | U62962 | Human Int-6 mRNA, complete cds. |
| 16 | CATG TTTTTGATAA A | -1048113 | D16891 | Human HepG2 3' region cDNA, clone hmd2c11. |
| 17 | CATG CAGCTGGCCA T | -302741 | X53743 | H.sapiens mRNA for fibulin-1 C. |

| | | | | | |
|---|---|---|---|---|---|
| 18 | CATG GTTCACATTA G | -774461 | X00497 | Human mRNA for HLA-DR antigens associated invarian | |
| | | | M13560 | Human Ia-associated invariant gamma-chain gene, ex | |
| 19 | CATG AAAAGAAACT T | -2056 | Y00345 | Human mRNA for polyA binding protein. | |
| 20 | CATG AATGCAGGCA G | -58533 | M61831 | Human S-adenosylhomocysteine hydrolase (AHCY) mRNA | |
| | | | M61832 | Human S-adenosylhomocysteine hydrolase (AHCY) mRNA | |
| 21 | CATG TGAAATAAAA C | -918273 | X16934 | Human hB23 gene for B23 nucleophosmin. | |
| | | | M28699 | Homo sapiens nucleolar phosphoprotein B23 (NPM1) m | |
| | | | M23613 | Human nucleophosmin mRNA, complete cds. | |
| | | | M26697 | Human nucleolar protein (B23) mRNA, complete cds. | |
| | | | | Human MHC protein homologous to chicken B complex | |
| 22 | CATG TTATGGGATC T | -998030 | M24194 | | |
| 23 | CATG CAATAAATGT T | -274492 | D23661 | Human mRNA for ribosomal protein L37, complete cds | |
| | | | L11567 | Homo sapiens ribosomal protein L37 mRNA, complete | |
| 24 | CATG AGCCTTTGTT G | -155632 | D83174 | Human mRNA for collagen binding protein 2. | |
| 25 | CATG ACCTGTATCC C | -97078 | X57352 | Human 1-8U gene from interferon-inducible gene fam | |
| 26 | CATG TTCAATAAAA A | -1000193 | M17886 | Human acidic ribosomal phosphoprotein P1 mRNA, com | |
| | | | J05068 | human transcobalamin I mRNA, complete cds. | |
| 27 | CATG CGACCCCACG C | -398663 | M12529 | Human apolipoprotein E mRNA, complete cds. | |
| | | | K00396 | Human apolipoprotein E (epsilon 2 and 3 alleles) m | |
| 28 | CATG CAGATCTTTG T | -298495 | X56998 | Human UbA52 adrenal mRNA for ubiquitin-52 amino ac | |
| | | | X56999 | Human UbA52 placental mRNA for ubiquitin-52 amino | |
| 29 | CATG CTGGCGAGCG C | -501287 | X07491 | Human DNA inserts showing sperm-specific hypomethy | |
| | | | M91670 | Human ubiquitin carrier protein (E2-EPF) mRNA, com | |
| 30 | CATG ATTGGCTTAA A | -256497 | L14272 | Human prohibitin (PHB) gene, exons 1-7. | |
| | | | S85655 | prohibitin (human, mRNA, 1043 nt). | |
| 31 | CATG GTGGTGGACA C | -765573 | U62435 | Human nicotinic acetylcholine receptor alpha6 subu | |
| | | | U68041 | Human breast and ovarian cancer susceptibility pro | |
| 32 | CATG TCCTGCCCCA T | -883029 | M24398 | Human parathymosin mRNA, complete cds. | |
| 33 | CATG ACTGGGTCTA T | -125661 | X58965 | H.sapiens RNA for nm23-H2 gene. | |
| | | | M36981 | Human putative NDP kinase (nm23-H2S) mRNA, complet | |
| | | | L16785 | Homo sapiens c-myc transcription factor (puf) mRNA | |
| 34 | CATG AAGAAGATAG A | -33331 | U02032 | Human ribosomal protein L23a mRNA, partial cds. | |
| | | | U37230 | Human ribosomal protein L23a mRNA, complete cds. | |
| | | | U43701 | Human ribosomal protein L23a mRNA, complete cds. | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | L13799 | Homo sapiens (clone 01) liver expressed protein mR | |
| 35 | CATG ACATCATCGA | T | -79065 | L06505 | Human ribosomal protein L12 mRNA, complete cds. | |
| 36 | CATG CTGTTGGTGA | T | -507577 | D14530 | Human homolog of yeast ribosomal protein S28, comp | |
| 37 | CATG ATTATTTTTC | T | -249854 | X57959 | H.sapiens mRNA for ribosomal protein L7. | |
| | | | | X57958 | H.sapiens mRNA for ribosomal protein L7. | |
| | | | | X52967 | Human mRNA for ribosomal protein L7. | |
| | | | | L16558 | Human ribosomal protein L7 (RPL7) mRNA, complete c | |
| 38 | CATG GCTTTTAAGG | A | -655115 | L06498 | Homo sapiens ribosomal protein S20 (RPS20) mRNA, c | |
| 39 | CATG GGCAAGAAGA | A | -672265 | L19527 | Homo sapiens ribosomal protein L27 (RPL27) mRNA, c | |
| | | | | L25346 | Homo sapiens ribosomal protein L27 (homologue of r | |
| 40 | CATG CTCTTCGAGA | A | -490889 | Y00433 | Human mRNA for glutathione peroxidase (EC 1.11.1.9 | |
| | | | | Y00483 | Human gene for gluthathione peroxidase. | |
| | | | | X13710 | H.sapiens unspliced mRNA for glutathione peroxidas | |
| | | | | X13709 | Human gpx1 mRNA for gluthatione peroxidase. | |
| | | | | M21304 | Human glutathione peroxidase (GPX1) mRNA, complete | |
| 41 | CATG CTGTTGATTG | C | -507455 | X04347 | Human liver mRNA fragment DNA binding protein UPI | |
| | | | | U00947 | Human clone C4E 3.2 (CAC)n/(GTG)n repeat-containin | |
| 42 | CATG CTGGGTTAAT | A | -502724 | M81757 | H.sapiens S19 ribosomal protein mRNA, complete cds | |
| 43 | CATG ATGGCTGGTA | T | -239533 | X17206 | Human mRNA for LLRep3. | |
| 44 | CATG GATGCTGCCA | A | -583573 | X59357 | Human mRNA for Epstein-Barr virus small RNAs (EBER | |
| | | | | L21756 | Homo sapiens acute myeloid leukemia associated pro | |
| | | | | D17652 | Human mRNA for HBp15/L22, complete cds. | |
| | | | | S76343 | AML1...EAP (translocation breakpoint) [human, chro | |
| 45 | CATG CCTTCGAGAT | C | -390692 | U14970 | Human ribosomal protein S5 mRNA, complete cds. | |
| 46 | CATG CTCCTCACCT | G | -482584 | U16811 | Human Bak mRNA, complete cds. | |
| | | | | U23765 | Human Bak protein mRNA, complete cds. | |
| 47 | CATG TGTGTTGAGA | G | -978825 | X16869 | Human mRNA for elongation factor 1-alpha (clone CE | |
| | | | | X16872 | Human DNA for elongation factor 1-alpha (clone lam | |
| | | | | X03558 | Human mRNA for elongation factor 1 alpha subunit ( | |
| | | | | D17182 | Human HepG2 3' region MboI cDNA, clone hmd2h03m3. | |
| | | | | D17245 | Human HepG2 3' region MboI cDNA, clone hmd4h05m3. | |
| | | | | D17259 | Human HepG2 3' region MboI cDNA, clone hmd5d07m3. | |
| | | | | D17276 | Human HepG2 3' region MboI cDNA, clone hmd6a12m3. | |

| | | | | | |
|---|---|---|---|---|---|
| | | | | M27364 | Human elongation factor 1 alpha mRNA, 3' end. |
| | | | | M29548 | Human e'ongation factor 1-alpha (EF1A) mRNA, parti |
| | | | | L41490 | Homo sapiens oncogene PTI-1 mRNA, complete cds. |
| | | | | L41498 | Homo sapiens oncogene PTI-1 mRNA, complete cds. |
| 48 | CATG TTACCATATC | A | -988366 | U57846 | Human ribosomal protein L39 mRNA, complete cds. |
| 49 | CATG GCCTGCTGGG | C | -621035 | X71973 | H.sapiens GPx-4 mRNA for phospholipid hydroperoxid |
| 50 | CATG CCTCGGAAAA | T | -383489 | Z26876 | H.sapiens gene for ribosomal protein L38. |
| 51 | CATG TACAAGAGGA | A | -803369 | X69391 | H.sapiens mRNA for ribosomal protein L6. |
| | | | -803369 | D17554 | Human mRNA for DNA-binding protein, TAXREB107, com |
| | | | -803369 | S71022 | neoplasm-related C140 product (human, thyroid carc |
| 52 | CATG AACGACCTCG | T | -24951 | V00598 | Human beta-tubulin pseudogene. |
| | | | -24951 | V00599 | Human mRNA fragment encoding beta-tubulin. (from c |
| 53 | CATG CCCTGCCTTG | T | -358783 | X55110 | Human mRNA for neurite outgrowth-promoting protein |
| 54 | CATG CCCAGGGAGA | A | -346761 | U38846 | Human stimulator of TAR RNA binding (SRB) mRNA, co |
| | | | | D16933 | Human HepG2 3' region cDNA, clone hmd4f11. |
| 55 | CATG AGCACCTCCA | G | -148949 | Z11692 | H.sapiens mRNA for elongation factor 2. |
| 56 | CATG CGCCGGAACA | C | -416261 | X73974 | H.sapiens HRPL4 mRNA. |
| | | | | D23660 | Human mRNA for ribosomal protein, complete cds. |
| 57 | CATG CTAAAAAAAA | A | -458753 | M33680 | Human 26-kDa cell surface protein TAPA-1 mRNA, com |
| 58 | CATG GGCTGATGTG | G | -686319 | U09510 | Human glycyl-tRNA synthetase mRNA, complete cds. |
| | | | | U09587 | Human glycyl-tRNA synthetase mRNA, complete cds. |
| | | | | D30658 | Human T-cell mRNA for glycyl tRNA synthetase, comp |
| 59 | CATG ATTCTCCAGT | A | -253260 | X55954 | Human mRNA for HL23 ribosomal protein homologue. |
| | | | | X52839 | Human mRNA for ribosomal protein L17. |
| 60 | CATG GAAAAATGGT | T | -524524 | X61156 | H.sapiens mRNA for laminin-binding protein. |
| | | | | X15005 | Human mRNA for potential laminin-binding protein ( |
| | | | | U43901 | Human 37 kD laminin receptor precursor/p40 ribosom |
| | | | | J03799 | Human colin carcinoma laminin-binding protein mRNA |
| | | | | M14199 | Human laminin receptor (2H5 epitope) mRNA, 5' end. |
| 61 | CATG CAGCTCACTG | A | -302367 | D87735 | Human mRNA for ribosomal protein L14, complete cds |
| | | | | L10376 | Human (clone CTG-B33) mRNA sequence. |
| | | | | S80520 | CAG-isl 7 (trinucleotide repeat-containing sequenc |
| 62 | CATG ATAATTCTTT | G | -200576 | U14973 | Human ribosomal protein S29 mRNA, complete cds. |

| | | | | | |
|---|---|---|---|---|---|
| | | | L31610 | Homo sapiens (clone cori-1c15) S29 ribosomal prote | |
| 63 | CATG AATCCTGTGG | A | -55227 | Z28407 | H.sapiens mRNA for ribosomal protein L8. |
| 64 | CATG AATAGGTCCA | A | -51925 | M64716 | Human ribosomal protein S25 mRNA, complete cds. |
| 65 | CATG AAAAAAAAA | A (C, G, T) | -1 | X83412 | H.sapiens B1 mRNA for mucin. |
| | | | | Z32564 | H.sapiens FRGAMMA mRNA (819bp) for folate receptor |
| | | | | Z32633 | H.sapiens FRGAMMA' mRNA for folate receptor (817bp |
| | | | | X76180 | H.sapiens mRNA for lung amiloride sensitive Na+ ch |
| | | | | U08470 | Human FR-gamma' mRNA, complete cds. |
| | | | | U08471 | Human folate receptor 3 mRNA, complete cds. |
| | | | | U48697 | Human mariner-like element-containing mRNA, clone |
| | | | | D28532 | Human mRNA for renal Na+-dependent phosphate cotra |
| | | | | M55914 | Human c-myc binding protein (MBP-1) mRNA, complete |
| | | | | L06175 | Homo Sapiens P5-1 mRNA, complete cds. |
| | | | | S73775 | calmitine=mitochondrial calcium-binding protein (h |
| | | | | S77393 | transcript ch138 (human, RF1,RF48 stomach cancer c |
| | | | | X60036 | H.sapiens mRNA for mitochondrial phosphate carrier |
| 66 | CATG CCAGAACAGA | C | -335945 | X79238 | H.sapiens mRNA for ribosomal protein L30. |
| | | | | L16991 | Human thymidylate kinase (CDC8) mRNA, complete cds |
| 67 | CATG AAGGTGGAGG | A | -44683 | X80822 | H.sapiens mRNA for ORF. |
| 68 | CATG CCTAGCTGGA | T | -379369 | X52856 | Human cyclophilin-related processed pseudogene. |
| | | | | X52857 | Human cyclophilin-related processed pseudogene. |
| | | | | X52854 | Human cyclophilin-related processed pseudogene. |
| | | | | X52851 | Human cyclophilin gene for cyclophilin (EC 5.2.1.8 |
| | | | | Y00052 | Human mRNA for T-cell cyclophilin. |
| 69 | CATG GAACACATCC | A | -528694 | X63527 | H.sapiens mRNA for ribosomal protein L19. |
| | | | | S56985 | ribosomal protein L19 (human, breast cancer cell 1 |
| 70 | CATG AAGGAGATGG | G | -41531 | X69181 | H.sapiens mRNA for ribosomal protein L31. |
| | | | | X15940 | Human mRNA for ribosomal protein L31. |
| 71 | CATG AGGCTACGGA | A | -171113 | Z29650 | H.sapiens SMCX mRNA. |
| | | | | D17233 | Human HepG2 3' region MboI cDNA, clone hmd4c12m3. |
| 72 | CATG AGGTCCTAGC | C | -177610 | X08096 | Human GST pi gene for glutathione S-transferase pi |

| | | | | |
|---|---|---|---|---|
| | | | X06547 | Human mRNA for class Pi glutathione S-transferase |
| | | | X15480 | Human mRNA for anionic glutathione-S-transferase ( |
| | | | X08058 | Human glutathione S-transferase pi gene. |
| | | | U12472 | Human glutathione S-transferase (GST phi) gene, co |
| | | | U21689 | Human glutathione S-transferase-P1c gene, complete |
| | | | U62589 | Human glutathione S-transferase P1c (GSTp1c) mRNA, |
| | | | M69113 | Human fatty acid ethyl ester synthase-III mRNA seq |
| | | | M24485 | Homo sapiens (clone pHGST-pi) glutathione S-transf |
| 73 | CATG TGGTGTTGAG G | -965603 | X69150 | H.sapiens mRNA for ribosomal protein S18. |
| | | | M96153 | Homo sapiens apolipoprotein B gene sequence. |
| | | | L06432 | Homo sapiens 18S ribosomal protein (HKE3) mRNA seq |
| 74 | CATG CTCAACATCT C | -475448 | M17885 | Human acidic ribosomal phosphoprotein P0 mRNA, com |
| 75 | CATG GTGTTAACCA G | -769045 | L25899 | Human ribosomal protein L10 mRNA, complete cds. |
| 76 | CATG AGGGCTTCCA A | -174037 | X58125 | Human (D9S55) DNA segment containing (TG)24 repeat |
| | | | D17260 | Human HepG2 3' region MboI cDNA, clone hmd5h09m3. |
| | | | M73791 | Human novel gene mRNA, complete cds. |
| | | | M64241 | Human Wilm's tumor-related protein (QM) mRNA, comp |
| | | | S35960 | laminin receptor homolog (3' region) [human, mRNA |
| 77 | CATG GGATTTGGCC T | -671654 | M17887 | Human acidic ribosomal phosphoprotein P2 mRNA, com |
| | | | M11147 | Human ferritin L chain mRNA, complete cds. |
| | | | M12938 | Human ferritin light subunit mRNA, partial cds. |
| | | | M10119 | Human ferritin light subunit mRNA, complete cds. |
| 78 | CATG ATTAACAAAG C | -246019 | X04409 | Human mRNA for coupling protein G(s) alpha-subunit |
| | | | X04408 | Human mRNA for coupling protein G(s) alpha subunit |
| | | | X56009 | Human GSA mRNA for alpha subunit of GsGTP binding |
| | | | X07036 | Human mRNA stimulatory GTP-binding protein alpha s |
| | | | M21142 | Human guanine nucleotide-binding protein alpha-sub |
| | | | M14631 | Human guanine nucleotide-binding protein G-s, alph |
| 79 | CATG TGTACCTGTA A | -968173 | Z36832 | H.sapiens (xs31) mRNA, 835bp. |
| | | | K00558 | human alpha-tubulin mRNA, complete cds. |
| 80 | CATG TGGCCCCACC C | -955718 | X56494 | H.sapiens M gene for M1-type and M2-type pyruvate |
| | | | M23725 | Human M2-type pyruvate kinase mRNA, complete cds. |
| | | | M26252 | Human TCB gene encoding cytosolic thyroid hormone- |

| | | | | | |
|---|---|---|---|---|---|
| 81 | CATG TAATAAAGGT | G | -798764 | X67247 | H.sapiens rpS8 gene for ribosomal protein S8. |
| 82 | CATG GCATAATAGG | T | -602315 | X89401 | H.sapiens mRNA for large subunit of ribosomal prot |
| | | | | U14967 | Human ribosomal protein L21 mRNA, complete cds. |
| | | | | U25789 | Human ribosomal protein L21 mRNA, complete cds. |
| | | | | L38826 | Homo sapiens L21 ribosomal protein gene, partial c |
| 83 | CATG TACCATCAAT | A | -807748 | X53778 | H.sapiens bng mRNA for uracil DNA glycosylase. |
| | | | | U34995 | Human normal keratinocyte substraction library mRN |
| | | | | J02642 | Human glyceraldehyde 3-phosphate dehydrogenase mRN |
| | | | | M36164 | Human glyceraldehyde-3-phosphate dehydrogenase mRN |
| | | | | M33197 | Human glyceraldehyde-3-phosphate dehydrogenase (GA |
| 84 | CATG ATTTGTCCCA | G | -260949 | X14957 | Human hmgI mRNA for high mobility group protein I. |
| | | | | X14958 | Human hmgI mRNA for high mobility group protein Y. |
| | | | | M23614 | Human HMG-I protein isoform mRNA (HMGI gene), clon |
| | | | | M23619 | Human HMG-I protein isoform mRNA (HMGI gene), clon |
| | | | | L17131 | Human high mobility group protein (HMG-I(Y)) gene |
| | | | | M23615 | Human HMG-Y protein isoform mRNA (HMGI gene), clon |
| | | | | M23616 | Human HMG-Y protein isoform mRNA (HMGI gene), clon |
| | | | | M23617 | Human HMG-Y protein isoform mRNA (HMGI gene), cloh |
| | | | | M23618 | Human HMG-Y protein isoform mRNA (HMGI gene), clon |
| 85 | CATG GAGGGAGTTT | C | -567488 | U14968 | Human ribosomal protein L27a mRNA, complete cds. |
| 86 | CATG CGCCGCCGGC | T | -416106 | U12465 | Human ribosomal protein L35 mRNA, complete cds. |
| 87 | CATG GTGAAACCCA | ALL | -753749 | Z63072 | H.sapiens CpG island DNA genomic Msel fragment, cl |
| 88 | CATG GTGAAACCCA | ALL | -753749 | X16294 | Human repetitive DNA containing interspersed repea |
| 89 | CATG AAGACAGTGG | C | -33979 | X66699 | H.sapiens mRNA for ribosomal protein L37a. |
| | | | | L06499 | Homo sapiens ribosomal protein L37a (RPL37A) mRNA, |
| | | | | L22154 | Human ribosomal protein L37a mRNA sequence. |
| 90 | CATG CCCCAGCCAG | T | -348755 | X55715 | Human Hums3 mRNA for 40S ribosomal protein s3. |
| | | | | U14990 | Human XP1PO ribosomal protein S3 (rpS3) mRNA, comp |
| | | | | U14991 | Human XP2NE ribosomal protein S3 (rpS3) mRNA, comp |
| | | | | U14992 | Human IMR-90 ribosomal protein S3 (rpS3) mRNA, com |
| | | | | S42658 | S3 ribosomal protein (human, colon, mRNA, 826 ntJ. |
| 91 | CATG TGGGCAAAGC | C | -959498 | X63526 | H.sapiens mRNA for protein homologous to elongatio |
| | | | | Z11531 | H.sapiens mRNA for elongation factor-1-gamma. |

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|---|---|---|---|---|---|---|
| | | | | M55409 | | Human pancreatic tumor-related protein mRNA, 3' en |
| 92 | CATG TGAGGAATA | A | -928269 | M10036 | | Human triosephosphate isomerase mRNA, complete cds |
| 93 | CATG GACGACACGA | G | -549145 | U58682 | | Human ribosomal protein S28 mRNA, complete cds. |
| | | | | M58458 | | Human ribosomal protein S4 (RPS4X) isoform mRNA, c |
| | | | | M22146 | | Human scar protein mRNA, complete cds. |
| 94 | CATG AACGCGGCCA | A | -26261 | Z23063 | | Homo sapiens macrophage migration inhibitory facto |
| | | | | L10612 | | Human glycosylation-inhibiting factor mRNA, comple |
| | | | | M95775 | | Homo sapiens macrophage migration inhibitory facto |
| | | | | L19686 | | Homo sapiens macrophage migration inhibitory facto |
| | | | | M25639 | | Human migration inhibitory factor (MIF) mRNA, comp |
| | | | | | | Human mRNA for ribosomal protein L32. |
| 95 | CATG TGCACGTTTT | C | -935680 | X03342 | | |
| | | | | K03002 | | Human mRNA from chromosome 15 gene with homology t |
| 96 | CATG CACAAACGGT | A | -278636 | U57847 | | Human ribosomal protein S27 mRNA, complete cds. |
| | | | | L19739 | | Homo sapiens metallopanstimulin (MPS1) mRNA, compl |
| 97 | CATG GGAGTGGACA | T | -667269 | L11566 | | Homo sapiens ribosomal protein L18 (RPL18) mRNA, c |
| 98 | CATG GCCGAGGAAG | G | -615043 | Z54999 | | H.sapiens CpG island DNA genomic Msel fragment, cl |
| | | | | Z57572 | | H.sapiens CpG island DNA genomic Msel fragment, cl |
| | | | | Z56073 | | H.sapiens CpG island DNA genomic Msel fragment, cl |
| | | | | X53505 | | Human mRNA for ribosomal protein S12. |
| 99 | CATG GGGGAAATCG | C | -696375 | M92381 | | Human thymosin beta 10 mRNA, complete cds. |
| | | | | M20259 | | Human thymosin beta-10 mRNA, complete cds. |
| 100 | CATG GCAGCCATCC | G | -599350 | U14969 | | Human ribosomal protein L28 mRNA, complete cds. |
| | | | | D17257 | | Human HepG2 3' region MboI cDNA, clone hmd5d04m3. |
| 101 | CATG TAAGGAGCTG | A | -796831 | X77770 | | H.sapiens RPS26 mRNA. |
| | | | | X69654 | | H.sapiens mRNA for ribosomal protein S26. |
| 102 | CATG GGCAAGCCCC | A | -672342 | U12404 | | Human Csa-19 mRNA, complete cds. |
| | | | | X79239 | | H.sapiens mRNA for ribosomal protein S13. |
| | | | | L01124 | | Human ribosomal protein S13 (RPS13) mRNA, complete |
| | | | | X65923 | | H.sapiens fau mRNA. |
| 103 | CATG GTTCCCTGGC | C | -775658 | U02523 | | Human FAU1P pseudogene, trinucleotide repeat regio |
| | | | | M60854 | | Human ribosomal protein S16 mRNA, complete cds. |
| 104 | CATG CCGTCCAAGG | G | -374027 | Z12962 | | H.sapiens mRNA for homologue to yeast ribosomal pr |
| | CATG TTGGTCCTCT | G | -1027448 | S64030 | | L41 ribosomal protein homolog (clone 7B6) [human, |

| | | | | | |
|---|---|---|---|---|---|
| 105 | CATG CAAACCATCC A | -263478 | X12883 | Human mRNA for cytokeratin 18. | |
| | | | X12876 | Human mRNA fragment for cytokeratin 18. | |
| | | | X12881 | Human mRNA for cytokeratin 18. | |
| | | | M24842 | Human keratin 18 (K18) gene, complete cds. | |
| | | | M26325 | Human cytokeratin 18 mRNA, 3' end. | |
| | | | M26326 | Human keratin 18 mRNA, complete cds. | |
| | | | M26327 | Human cytokeratin 18 mRNA, 3' end. | |
| 106 | CATG AGCTCTCCCT G | -161624 | X53777 | Human L23 mRNA for putative ribosomal protein. | |
| 107 | CATG AGGTCAGGAG A(T) | -177315 | D86979 | Human male bone marrow myeloblast mRNA for KIAA022 | |
| | | | X55923 | Human DNA for Alu element PIN6. | |
| | | | X79699 | H.sapiens ALU repeat, 230bp. | |
| | | | X12544 | Human mRNA for HLA class II DR-beta (HLA-DR B). | |
| | | | Z77989 | H.sapiens flow-sorted chromosome 6 HindIII fragmen | |
| | | | U11831 | Human clone 2102V-I chromosome 18p telomeric seque | |
| | | | U12580 | Human Alu repeat sequence A3. | |
| | | | U12582 | Human Alu repeat sequence B2. | |
| | | | U12583 | Human Alu repeat sequence D1. | |
| | | | U14694 | Human Alu-Sb2 repeat, clone HALUSB08. | |
| | | | U14695 | Human Alu-Sb2 repeat, clone HALUSB15. | |
| | | | U14696 | Human Alu-Sb2 repeat, clone HALUSB27. | |
| | | | U14697 | Human Alu-Sb2 repeat, clone HUM-11. | |
| | | | U14698 | Human Alu-Sb2 repeat, clone HSB-8P. | |
| | | | U14699 | Human Alu-Sb2 repeat, clone HUM-9. | |
| | | | U14700 | Human Alu-Sb2 repeat, clone HALUSB35. | |
| | | | U14701 | Human Alu-Sb2 repeat, clone HSB-2P. | |
| | | | U14704 | Human Alu-Sb2 repeat, clone HUM-3. | |
| | | | U14706 | Human Alu-Sb2 repeat, clone HUM-10. | |
| | | | U14707 | Human Alu-Sb2 repeat, clone HUM-7. | |
| | | | J00120 | Human (Lawn) c-myc proto-oncogene, complete coding | |
| | | | L34653 | Homo sapiens platelet/endothelial cell adhesion mo | |
| | | | M37521 | Human XV2c gene. | |
| | | | S61789 | NF1=neurofibromatosis type 1 (deletion breakpoint, | |
| | | | S73483 | phosphorylase kinase catalytic subunit PHKG2 homol | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | S75201 | cholinesterase (Alu element) [human, Insertion Mut |
| | | | | S75337 | (Y Alu polymorphism, YAP, polymorphic subfamily-3) |
| 108 | CATG GGGCTGGGGT | C | -695980 | Z49148 | H.sapiens mRNA for ribosomal protein L29. |
| | | | | U10248 | Human ribosomal protein L29 (humrpl29) mRNA, compl |
| | | | | U49083 | Human cell surface heparin binding protein HIP mRN |
| | | | | D16992 | Human HepG2 partial cDNA, clone hmd2d02m5. |
| | | | | D16911 | Human HepG2 3' region cDNA, clone hmd3b09. |
| | | | | J03537 | Human ribosomal protein S6 mRNA, complete cds. |
| | | | | M20020 | Human ribosomal protein S6 mRNA, complete cds. |
| 109 | CATG ACGTTCTCTT | C | -114144 | | EST |
| 110 | CATG TCTCCATACC | C | -906438 | | EST |
| 111 | CATG GACTGCGTGC | C | -555450 | | EST |
| 112 | CATG CTTAATCCTG | A | -508767 | | EST |
| 113 | CATG GGTTGGCAGG | G | -719435 | | EST |
| 114 | CATG GCCCTCTGCC | A | -613862 | | EST |
| 115 | CATG AACAGAAGCA | A | -18469 | | EST |
| 116 | CATG CTGCCGAGCT | C | -497192 | | EST |
| 117 | CATG TTCCTCGGGC | A | -1007018 | | EST |
| 118 | CATG AACTAATACT | A | -28872 | | EST |
| 119 | CATG TAGATAATGG | C | -822331 | | EST |
| 120 | CATG GCCACACCCC | A,C | -607318 | | EST |
| 121 | CATG GAACCCTGGG | A | -529899 | | EST |
| 122 | CATG AACTAAAAAA | A | -28673 | | EST |
| 123 | CATG GAAATGTAAG | A | -528067 | | EST |
| 124 | CATG ACTCCAAAAA | A | -119809 | | EST |
| 125 | CATG GTTCGTGCCA | A | -777109 | | EST |
| 126 | CATG TTACCTCCTT | C | -989024 | | EST |
| 127 | CATG GCACAAGAAG | A | -594051 | | EST |
| 128 | CATG CCCTGGGTTC | T | -359102 | | EST |
| 129 | CATG GCCTGTATGA | G | -621369 | | EST |
| 130 | CATG CCCGTCCGGA | A | -355689 | | EST |
| 131 | CATG AGGAAGCTG | C | -163999 | | EST |
| 132 | CATG TCAGATCTTT | G | -861056 | | EST |

| | | | | |
|---|---|---|---|---|
| 133 | CATG CCAGGAGGAA | T | -338081 | EST |
| 134 | CATG TCACCCACAC | C | -857362 | EST |
| 135 | CATG GTGTTGCACA | A | -769605 | EST |
| 136 | CATG GCCGTGTCCG | C | -618199 | EST |

Isolation of partial cDNA (3' fragment) by 3' directed PCR reaction

This procedure is a modification of the protocol described in Polyak et al. (1997) Nature 389:300. Briefly, the procedure uses SAGE tags in PCR reaction such that the resultant PCR product contains the SAGE tag of interest as well as additional cDNA, the length of which is defined by the position of the tag with respect to the 3' end of the cDNA. The cDNA product derived from such a transcript driven PCR reaction can be used for many applications.

RNA from a source believed to express the cDNA corresponding to a given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to dreive the first strand synthesis. For example, the oligonucleotide of compositon 5'-B-TCC GGC GCG CCG TTT T CC CAG TCA CGA(30)-3', contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the streptavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

cDNA constructed utilizing this or similar modified oligo-dT primer is then processed exactly as described in U.S. Patent No. (insert) up until adapter ligation where only one adapter is ligated to the cDNA pool. After adapter ligation, the cDNA is released from the streptavidin-coated magnetic beads and is then used as a template for cDNA amplification.

Various PCR protocols can be employed using PCR priming sites within the 3' modified oligo-dT primer and the SAGE tag. The SAGE tag-derived PCR primer employed can be of varying length dictated by 5' extension of the tag into the adaptor sequence. cDNA products are now available for a variety of applications.

This technique can be further modified by: (1) altering the length and/or content of the modified oligo-dT primer; (2) ligating adaptors other than that previously employed within the SAGE protocol; (3) performing PCR from template retained on the streptavidin-coated magnetic beads; and (4) priming first strand cDNA synthesis with non-oligo-dT based primers.

Isolation of cDNA using GeneTrapper or modified GeneTrapper Technology

The reagents and manufacturer's instructions for this technology are commercially available from Life Technologies, Inc., Gaithersburg, Maryland. Briefly, a complex population of single-stranded phagemid DNA containing directional cDNA inserts is enriched for the target sequence by hybridization in solution to a biotinylated oligonucleotide probe complementary to the target sequence. The hybrids are captured on streptavidin-coated paramagnetic beads. A magnet retrieves the paramagnetic beads from the solution, leaving nonhybridized single-stranded DNAs behind. Subsequently, the captured single-stranded DNA target is released from the biotinylated oligonucleotide. After release, the cDNA clone is further enriched by using a nonbiotinylated target oligonucleotide to specifically prime conversion of the single-stranded target to double-stranded DNA. Following transformation and plating, typically 20% to 100% of the colonies represent the cDNA clone of interest. To identify the desired cDNA clone, the colonies may be screened by colony hybridization using the 32P-labeled oligonucleotide as described above for solution hybridization, or alternatively by DNA sequencing and alignment of all sequences obtained from numerous clones to determine a consensus sequence.

The genes which are identified herein as being differentially expressed in normal and cancer cells can be used diagnostically and prognostically. Transcription levels in a test sample suspected of being neoplastic can be determined and compared to the levels in normal colon cells. The test sample may be from any tissue suspected of neoplasia, and particularly from either suspected colorectal or suspected pancreatic cancer cells. The control cells for

the purposes of comparison are normal cells, preferably of the same tissue type as the test sample, *e.g.*, colon cells, or pancreatic duct epithelial cells. Upregulation of transcription or downregulation of transcription is therefore diagnostic of the neoplastic state, depending on what gene is used as a test reagent. Similarly, transcription levels can be monitored to assess patent responses to anti-tumor therapies. Transcription levels will also provide prognostic information. For example, the level of transcription in a test sample can be compared to levels found in *bona fide* normal and tumor cells. More extreme deviations from normal expression levels indicate a poorer prognosis.

Transcription levels can be determined according to any means known in the art. These include, without limitation, Northern blots, nuclear run-on assays, *in vitro* transcription assays, primer extension assays, quantitative reverse transcriptase-polymerase chain reactions (RT-PCR), and hybrid filter binding assays. These techniques are well known in the art. See J.C. Alwine, D.J. Kemp, G.R. Stark, *Proc. Natl. Acad. Sci. U.S.A.* 74, 5350 (1977); K. Zinn, D. Di-Maio, T. Maniatis, *Cell* 34, 865 (1983); G. Veres, R.A. Gibbbs, S.E. Scherer, C.T. Caskey, *Science* 237, 415 (1987).

Similarly, upregulated genes and downregulated genes can be detected by measuring expression of their protein products. This can be done by any means known in the art, including but not limited to Western (immuno) blot, enzyme linked immunoadsorbent assay, radioimmunoassay, and enzyme assay. Such techniques are well known in the art. Protein products can be detected in tissue samples of a test patient, using a suspect sample as a test sample, and a matched normal tissue sample from the same tissue type as a control. If normal tissue is not available then a closely related tissue type can be used. Desirably both the samples being compared will be from the same individual. Alternatively, aberrant expression levels of protein products can be detected in body samples, such as blood, serum, feces, urine, sputum. As a control, a normal matched sample can be used from a healthy individual. Aberrant expression levels of transcripts can also be detected in such body samples, particularly in blood and serum.

Probes for use in the assays for transcription levels of particular genes or sets of genes may be RNA or DNA. The probes will be isolated substantially free of other cellular RNAs or DNAs. If the reagent contains one probe then it will comprise at least 50% of the nucleic acids in the reagent composition. If the reagent contains more than one probe, then the proportion will decrease accordingly, so that specific probes will still comprise at least 50% of the nucleic acids in the reagent composition.

Probes can be labeled according to any means known in the art. These may include radioactive labels, fluorescent labels, enzymatic labels, and binding partner labels such as biotin. Means for labeling and detecting probes are well known in the art. Probes comprise at least 10, 11, 12, 15, 20, or 30 contiguous nucleotides of a selected gene.

This invention provides proteins or polypeptides expressed from the polynucleotides of this invention, which is intended to include wild-type and recombinantly produced polypeptides and proteins from procaryotic and eucaryotic host cells, as well as muteins, analogs and fragments thereof. In some embodiments, the term also includes antibodies and anti-idiotypic antibodies.

It is understood that functional equivalents or variants of the wild-type polypeptide or protein also are within the scope of this invention, for example, those having conservative amino acid substitutions. Other analogs include fusion proteins comprising a protein or polypeptide.

The proteins and polypeptides of this invention are obtainable by a number of processes well known to those of skill in the art, which include purification, chemical synthesis and recombinant methods. Full length proteins can be purified from a colon or pancreatic cell or tissue lysate by methods such as immunoprecipitation with antibody, and standard techniques such as gel filtration, ion-exchange, reversed-phase, and affinity chromatography using a fusion protein as shown herein. For such methodology, see for example Deutscher et al. (1999) Guide To Protein Purification: Methods In Enzymology (Vol. 182, Academic Press). Accordingly, this invention also

provides the processes for obtaining these proteins and polypeptides as well as the products obtainable and obtained by these processes.

The proteins and polypeptides also can be obtained by chemical synthesis using a commercially available automated peptide synthesizer such as those manufactured by Perkin Elmer/Applied Biosystems, Inc., Model 430A or 431A, Foster City. The synthesized protein or polypeptide can be precipitated and further purified, for example by high performance liquid chromatography (HPLC). Accordingly, this invention also provides a process for chemically synthesizing the proteins of this invention by providing the sequence of the protein and reagents, such as amino acids and enzymes and linking together the amino acids in the proper orientation and linear sequence.

Alternatively, the proteins and polypeptides can be obtained by well-known recombinant methods as described, for example, in Sambrook et al., (1989), supra, using the host cell and vector systems described above.

Also provided by this application are the polypeptides and proteins described herein conjugated to a detectable agent for use in the diagnostic methods. For example, detectably labeled proteins and polypeptides can be bound to a column and used for the detection and purification of antibodies. They also are useful as immunogens for the production of antibodies as described below. The proteins and fragments of this invention are useful in an in vitro assay system to screen for agents or drugs, which modulate cellular processes.

The proteins of this invention also can be combined with various liquid phase carriers, such as sterile or aqueous solutions, pharmaceutically acceptable carriers, suspensions and emulsions. Examples of non-aqueous solvents include propyl ethylene glycol, polyethylene glycol and vegetable oils. When used to prepare antibodies, the carriers also can include an adjuvant that is useful to non-specifically augment a specific immune response. A skilled artisan can easily determine whether an adjuvant is required and select one. However, for the purpose of illustration only, suitable adjuvants include, but

are not limited to Freund's Complete and Incomplete, mineral salts and polynucleotides.

This invention also provides a pharmaceutical composition comprising any of a protein, analog, mutein, polypeptide fragment, antibody, antibody fragment or anti-idiotipic antibody of this invention, alone or in combination with each other or other agents, and an acceptable carrier. These compositions are useful for various diagnostic and therapeutic methods.

Antibodies can be generated using the proteins encoded by the transcripts identified by the tags disclosed herein. Use of all or portions of the protein as immunogens is routine in the art. Similarly, fusion proteins can be used as immunogens. Antibodies can be affinity purified using the proteins or portions thereof used as immunogens. Similarly, monoclonal antibodies specifically immunoreactive with the protein sequences of the invention can be generated according to techniques which are well known in the art.

Antibodies can be used analytically to quantitate the expression of particular transcripts identified herein as upregulated or downregulated in cancer. In addition, antibodies can be conjugated or non-covalently linked to cytotoxic agents, such as cytotoxins, radionuclides, chemotherapeutic drugs, etc. Such antibodies can be used therapeutically to specifically target cancer cells in which the protein antigens are upregulated. These include the proteins encoded by the transcripts identified by the tags shown in Tables 2, 4, and 5. Means of making such linked cytotoxic antibodies and of administering the same are well known in the art.

Also provided by this invention is an antibody capable of specifically forming a complex with the proteins or polypeptides as described above. The term "antibody" includes polyclonal antibodies and monoclonal antibodies. The antibodies include, but are not limited to mouse, rat, and rabbit or human antibodies.

Laboratory methods for producing polyclonal antibodies and monoclonal antibodies, as well as deducing their corresponding nucleic acid sequences, are known in the art, see Harlow and Lane (1988) supra and

Sambrook et al. (1989) supra. The monoclonal antibodies of this invention can be biologically produced by introducing protein or a fragment thereof into an animal, e.g., a mouse or a rabbit. The antibody producing cells in the animal are isolated and fused with myeloma cells or heteromyeloma cells to produce hybrid cells or hybridomas. Accordingly, the hybridoma cells producing the monoclonal antibodies of this invention also are provided.

Thus, using the protein or fragment thereof, and well known methods, one of skill in the art can produce and screen the hybridoma cells and antibodies of this invention for antibodies having the ability to bind the proteins or polypeptides.

If a monoclonal antibody being tested binds with the protein or polypeptide, then the antibody being tested and the antibodies provided by the hybridomas of this invention are equivalent. It also is possible to determine without undue experimentation, whether an antibody has the same specificity as the monoclonal antibody of this invention by determining whether the antibody being tested prevents a monoclonal antibody of this invention from binding the protein or polypeptide with which the monoclonal antibody is normally reactive. If the antibody being tested competes with the monoclonal antibody of the invention as shown by a decrease in binding by the monoclonal antibody of this invention, then it is likely that the two antibodies bind to the same or a closely related epitope. Alternatively, one can pre-incubate the monoclonal antibody of this invention with a protein with which it is normally reactive, and determine if the monoclonal antibody being tested is inhibited in its ability to bind the antigen. If the monoclonal antibody being tested is inhibited then, in all likelihood, it has the same, or a closely related, epitopic specificity as the monoclonal antibody of this invention.

The term "antibody" also is intended to include antibodies of all isotypes. Particular isotypes of a monoclonal antibody can be prepared either directly by selecting from the initial fusion, or prepared secondarily, from a parental hybridoma secreting a monoclonal antibody of different isotype by using the sib selection technique to isolate class switch variants using the

procedure described in Steplewski et al. (1985) Proc. Natl. Acad. Sci. 82:8653 or Spira et al. (1984) J. Immunol. Methods 74:307.

This invention also provides biological active fragments of the polyclonal and monoclonal antibodies described above. These "antibody fragments" retain some ability to selectively bind with its antigen or immunogen. Such antibody fragments can include, but are not limited to:

(1) Fab,

(2) Fab',

(3) F(ab')2,

(4) Fv, and

(5) SCA

A specific example of "a biologically active antibody fragment" is a CDR region of the antibody. Methods of making these fragments are known in the art, see for example, Harlow and Lane, (1988) supra.

The antibodies of this invention also can be modified to create chimeric antibodies and humanized antibodies (Oi, et al. (1986) BioTechniques 4(3):214). Chimeric antibodies are those in which the various domains of the antibodies' heavy and light chains are coded for by DNA from more than one species.

The isolation of other hybridomas secreting monoclonal antibodies with the specificity of the monoclonal antibodies of the invention can also be accomplished by one of ordinary skill in the art by producing anti-idiotypic antibodies (Herlyn, et al. (1986) Science 232:100). An anti-idiotypic antibody is an antibody which recognizes unique determinants present on the monoclonal antibody produced by the hybridoma of interest.

Idiotypic identity between monoclonal antibodies of two hybridomas demonstrates that the two monoclonal antibodies are the same with respect to their recognition of the same epitopic determinant. Thus, by using antibodies to the epitopic determinants on a monoclonal antibody it is possible to identify other hybridomas expressing monoclonal antibodies of the same epitopic specificity.

It is also possible to use the anti-idiotype technology to produce monoclonal antibodies which mimic an epitope. For example, an anti-idiotypic monoclonal antibody made to a first monoclonal antibody will have a binding domain in the hypervariable region which is the mirror image of the epitope bound by the first monoclonal antibody. Thus, in this instance, the anti-idiotypic monoclonal antibody could be used for immunization for production of these antibodies.

As used in this invention, the term "epitope" is meant to include any determinant having specific affinity for the monoclonal antibodies of the invention. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics.

The antibodies of this invention can be linked to a detectable agent or label. There are many different labels and methods of labeling known to those of ordinary skill in the art.

The antibody-label complex is useful to detect the protein or fragments in a sample, using standard immunochemical techniques such as immunohistochemistry as described by Harlow and Lane (1988) supra. Competitive and non-competitive immunoassays in either a direct or indirect format are examples of such assays, e.g., enzyme linked immunoassay (ELISA) radioimmunoassay (RIA) and the sandwich (immunometric) assay. Those of skill in the art will know, or can readily discern, other immunoassay formats without undue experimentation.

The coupling of antibodies to low molecular weight haptens can increase the sensitivity of the assay. The haptens can then be specifically detected by means of a second reaction. For example, it is common to use haptens such as biotin, which reacts avidin, or dinitropherryl, pyridoxal, and fluorescein, which can react with specific anti-hapten antibodies. See Harlow and Lane (1988) supra.

The monoclonal antibodies of the invention also can be bound to many different carriers. Thus, this invention also provides compositions containing the antibodies and another substance, active or inert. Examples of well-known carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magnetite. The nature of the carrier can be either soluble or insoluble for purposes of the invention. Those skilled in the art will know of other suitable carriers for binding monoclonal antibodies, or will be able to ascertain such, using routine experimentation.

Compositions containing the antibodies, fragments thereof or cell lines which produce the antibodies, are encompassed by this invention. When these compositions are to be used pharmaceutically, they are combined with a pharmaceutically acceptable carrier.

The present invention also provides a screen for various agents which modulate the expression of a gene in a pancreatic or colon cell. To practice the method in vitro, suitable cell cultures or tissue cultures are first provided. The cell can be a cultured cell or a genetically modified cell in which a trancript from SEQ ID NOS:1-732, or their complements, is expressed. Alternatively, the cells can be from a tissue biopsy. The cells are cultured under conditions (temperature, growth or culture medium and gas ($CO_2$)) and for an appropriate amount of time to attain exponential proliferation without density dependent constraints. It also is desirable to maintain an additional separate cell culture; one which does not receive the agent being tested as a control.

As is apparent to one of skill in the art, suitable cells may be cultured in microtiter plates and several agents may be assayed at the same time by noting genotypic changes, phenotypic changes or cell death.

When the agent is a composition other than a DNA or RNA, the agent may be directly added to the cell culture or added to culture medium for addition. As is apparent to those skilled in the art, an "effective" amount must be added which can be empirically determined. When the agent is a polynucleotide, it may be directly added by use of a gene gun or

electroporation. Alternatively, it may be inserted into the cell using a gene delivery vehicle or vector as described above.

An agent is a potential therapeutic if it alters the expression of gene in the cell. Altered expression can be detected by assaying for altered mRNA expression or protein expression using the probes, primers and antibodies as described herein.

For the purposes of this invention, an "agent" is intended to include, but not be limited to a biological or chemical compound such as a simple or complex organic or inorganic molecule, a peptide, a protein (e.g. antibody) or a polynucleotide (e.g. anti-sense). A vast array of compounds can be synthesized, for example polymers, such as polypeptides and polynucleotides, and synthetic organic compounds based on various core structures, and these are also included in the term "agent". In addition, various natural sources can provide compounds for screening, such as plant or animal extracts, and the like. It should be understood, although not always explicitly stated that the agent is used alone or in combination with another agent, having the same or different biological activity as the agents identified by the inventive screen. The agents and methods also are intended to be combined with other therapies.

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

This example demonstrates the characterization of the general transcription of human colorectal epithelium, colorectal cancers, and pancreatic cancers.

We used the recently developed SAGE (serial analysis of gene expression) method to identify and quantify a total of 303,706 transcripts derived from human colorectal (CR) epithelium, CR cancers or pancreatic cancers (Table 1A ) (*3*). These transcripts represented approximately 48,741

different genes (4) that ranged in average expression from 1 copy per cell to as many as 5,300 copies per cell (5). The number of different transcripts observed in each cell population varied from 14,247 to 20,471. The bulk of the mRNA mass (75%) consisted of transcripts expressed at more than five copies per cell on average (Table 1B). In contrast, the majority (86%) of transcripts were expressed at less than 5 copies per cell, but in aggregate this low abundance class represented only 25% of the mRNA mass. This distribution was consistently observed among the different samples analyzed and was consistent with previous studies of RNA abundance classes based on RNA-DNA reassociation kinetics (Rot curves). Monte Carlo simulations revealed that our analyses had a 92% probability of detecting a transcript expressed at an average of three copies per cell (7).

Table 1 - Summary of SAGE Analysis

A. Overall Summary

| | Normal Colon | Colon Tumors | Colon Cell Lines | Pancreatic Tumors | Pancreatic Cell Lines | Total |
|---|---|---|---|---|---|---|
| **Total Tags** | 62,168 | 60,878 | 60,373 | 61,592 | 58,695 | 303,706 |
| **Unique Genes**[1] | 14,721 | 19,690 | 17,092 | 20,471 | 14,247 | 48,741 |
| **GenBank**[2] | 8,753 (59) | 10,490 (53) | 10,193 (60) | 11,547 (56) | 8,922 (63) | 26,339 (54) |

[1] Indicates the number of different genes represented by the total tags analyzed (4).

[2] Indicates the number of genes that matched an entry in GenBank. The number in parentheses indicates the corresponding percentage of total unique tags.

Table 1 - Summary of SAGE Analysis

**B. Summarized by Abundance Classes***

| Copies/Cell | Normal Colon | Colon Tumors | Colon Cell Lines | Pancreatic Tumors | Pancreatic Cell Lines | Total |
|---|---|---|---|---|---|---|
| > 500 | | | | | | |
| Unique Genes | 62 (29) | 54 (25) | 54 (19) | 32 (11) | 70 (26) | 55 (19) |
| GenBank | 59 (95) | 52 (96) | 53 (98) | 32 (100) | 70 (100) | 54 (98) |
| > 50 and ≤ 500 | | | | | | |
| Unique Genes | 645 (28) | 470 (21) | 618 (27) | 657 (29) | 585 (27) | 595 (26) |
| GenBank | 545 (84) | 429 (91) | 579 (94) | 609 (93) | 529 (90) | 553 (93) |
| > 5 and ≤ 50 | | | | | | |
| Unique Genes | 4,569 (27) | 5,011 (29) | 5,733 (34) | 6,146 (36) | 4,895 (31) | 6,209 (30) |
| GenBank | 2,893 (63) | 3,204 (64) | 3,682 (64) | 4,054 (66) | 3,168 (65) | 4,241 (68) |

| ≤ 5 | | | | | | |
|---|---|---|---|---|---|---|
| Unique Genes | 9,445 (16) | 14,155 (25) | 10,687 (20) | 13,636 (24) | 8,697 (16) | 41,882 (25) |
| GenBank | 5,256 (56) | 6,805 (48) | 5,879 (55) | 6,852 (50) | 5,155 (59) | 21,491 (51) |

*For unique genes, the first number denotes the number of different genes (4) represented in the indicated abundance class. The number in parentheses indicates the mass fraction (X100) of total transcripts represented by the indicated abundance class. For GenBank entries, the first number indicates the number of different genes that matched an entry in GenBank in the indicated abundance class. The number in parentheses indicates the corresponding percentage of total genes.

Many of the SAGE tags appeared to represent previously undescribed transcripts, as only 54% of the tags matched entries in GenBank (Table 1). Twenty percent of these matching transcripts corresponded to characterized mRNA sequence entries in GenBank, whereas 80% matched uncharacterized EST entries. As expected, the likelihood of a tag being present in the databases was related to abundance; GenBank matches were identified for 98% of the transcripts expressed at more than 500 copies per cell but for only 51% of the transcripts expressed at $\leq 5$ copies per cell. Because the SAGE data provide a quantitative assay of transcript abundance, unaffected by differences in cloning or PCR efficiency, these data provide an independent and relatively unbiased estimate of the current completeness of publicly available EST databases.

## EXAMPLE 2

This example demonstrates a comparison of the expression pattern of normal colon epithelium and primary colon cancers.

Comparison of expression patterns between normal colon epithelium and primary colon cancers revealed that the majority of transcripts were expressed at similar levels (Fig. 1A). However, the expression profiles also revealed 289 transcripts that were expressed at significantly different levels [$P < 0.01$, (8)]. Of these 289, 181 were decreased in colon tumors compared to normal colon (average decrease 10-fold; Fig. 1B; examples in Fig. 2A). Conversely, 108 transcripts were expressed at higher levels in the colon cancers than in normal colon (average increase 13-fold; Fig. 1C; examples in Fig. 2A). Monte Carlo simulations indicated that the analysis would have detected over 95% of those transcripts expressed at a 6-fold or greater level in normal vs. tumor cells or vice versa (*9*). Because relatively stringent criteria were used for defining differences [$P < 0.01$, (*8*)], the number of differences reported above is likely to be an underestimate.

EXAMPLE 3

This example demonstrates the similarities and differences between cancer cell line transcription and transcription of primary cancer tissues. To determine how many of the 289 differences were independent of the cellular microenvironment of cancers *in vivo*, SAGE data from CR cancer cell lines was compared to that from primary CR cancer tissues (Fig. 1B, 1C). Perhaps surprisingly, the majority of transcripts (130 of 181) that were expressed at reduced levels in cancer cells in vivo were also expressed at significantly lower levels in the cell lines (Fig. 1B). Likewise, a significant fraction of the transcripts expressed at increased levels in primary cancers were also expressed at higher levels in the CR cancer cell lines (Fig. 1C). Thus, many of the gene expression differences that distinguish normal from tumor cells in vivo persist during in vitro growth. However, despite these similarities there were also many differences. For example, only 47 of 228 genes expressed at higher levels in CR cancer cell lines were also expressed at high levels in the primary CR cancers.

In combination, comparing the expression pattern of CR cancer cells (in vivo or in vitro) to normal colon revealed 548 differentially expressed transcripts (Fig. 1B,C, Tables 2 and 3). The average difference in expression for these transcripts was 15 fold. Although the ability to detect differences is influenced by the magnitude of the variance with the power to detect smaller differences being less, 92 transcripts that were less than three fold different were identified among the 548 transcripts. However, those genes exhibiting the greatest differences in expression are likely to be the most biologically important.

EXAMPLE 4

This example demonstrates the similarities and differences between colorectal cancer transcription and pancreatic cancer transcription.

To determine whether the changes noted in CR cancers were neoplasia or cell type specific, we performed SAGE on mRNA derived from pancreatic cancers. A total of 404 transcripts were expressed at higher levels in pancreatic cancers compared to normal colon epithelium (examples in Fig. 2B). The majority (268) of these transcripts were pancreas-specific (*10*) (Example in Fig. 2C) although 136 were also expressed at high levels in CR cancers. These 136 transcripts constituted 47% of the 289 transcripts increased in CR cancers relative to normal colon and are likely to be related to the neoplastic process rather than to the specific cell type of origin.

EXAMPLE 5

This example demonstrates the reproducibility of the transcription patterns observed among a larger number of cancer samples.

One question that arose from these data is the potential heterogeneity of expression between individual tumors. The SAGE data were acquired from two examples of each tissue type (normal colon, primary CR cancer, CR cancer cell line, etc.). To examine the generality of these expression profiles, we arbitrarily selected 27 differentially expressed transcripts and evaluated them in six to twelve samples of normal colon and primary cancers by Northern blot analysis (*11*). In general, expression patterns were very reproducible among different samples. Of 10 genes with elevated expression in normal colon relative to CR cancers as determined by SAGE, each was detected in the normal colon samples and was expressed at considerably lower levels in tumors (examples in Fig. 2A). Similarly, most of the genes identified by SAGE as increased in CR or pancreatic cancers were confirmed to be reproducibly expressed in the majority of primary cancers examined by Northern blot (examples in Fig. 2A). It is important to note, however, that there were differences among the cancers, with a few cancers exhibiting particularly high or low levels of individual transcripts. Such differences in gene expression

undoubtedly contribute to the observed heterogeneity in biological properties of cancers derived from the same organ .

## EXAMPLE 6

This example demonstrates the identities of some of the transcripts which were found to be differentially expressed in tumor and normal tissues. What are the identities of the differentially expressed genes? Of the 548 differentially expressed transcripts, 337 were tentatively identified through database comparisons. When tested, the great majority (93%) of these identifications proved to be legitimate (*13*), as expected from previous SAGE analyses . Although a large number of differentially expressed genes were identified, some simple patterns did emerge. For example, genes that were expressed at higher levels in normal colon epithelium than in CR tumors were often differentiation-related. These genes included liver fatty acid binding protein , cytokeratin 20 , carbonic anhydrase , guanylin and uroguanylin , which are known to be important for the normal physiology or architecture of the colon epithelium (Table 2). On the other hand, genes that were increased in CR cancers were often related to the robust growth characteristics that these cells exhibit. For example, gene products associated with protein synthesis, including 48 ribosomal proteins, five elongation factors, and five genes involved in glycolysis were observed to be elevated in both CR and pancreatic cancers compared to normal colon cells. Although the majority of the transcripts could not have been predicted to be differentially expressed in cancers, several have previously been shown to be dysregulated in neoplastic cells. The latter included IGFII , B23 nucleophosmin, the Pi form of glutathione S-transferase, and several ribosomal proteins which were all increased in cancer cells as previously reported. Likewise, Dra and gelsolin were both decreased in cancer as previously reported. Surprisingly, two widely studied oncogenes, *c-fos* and *c-erbb3*, were expressed at much higher levels in normal colon epithelium than CR cancers, in contrast to their up-regulation in transformed cells .

In summary, these data provide basic information necessary for understanding the gene expression differences that underlie cancer phenotypes. They additionally provide a necessary framework for interpreting the significance of individual differentially expressed genes. Although this study demonstrated that a large number of such differences exist (approximately 500 at the depth of analysis employed), it was equally remarkable that the fraction of transcripts exhibiting significant differences was relatively small, representing 1.5 % of the transcripts detected in any given cell type (*26*). The fact that many, but not all, of the differences were preserved during in vitro culture demonstrates the utility of cultured lines for examination of some aspects of gene expression, but also provides a note of caution in relying on such lines to perfectly mimic tumors in their natural environment. Finally, the finding that hundreds of specific genes are expressed at different levels in CR cancers, and that some of these are also expressed differentially in pancreatic cancers, provides a wealth of new reagents for future biologic and diagnostic experimentation.

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3. To minimize individual variation, approximately equal numbers of tags (30,000) were derived from two different patients for each tissue. For primary tumors (two CR carcinomas and two pancreatic adenocarcinomas), RNA was isolated from portions of tumors judged to contain 60%-90% tumor cells by histopathology. The cells grown in vitro were derived from CR (SW837, Caco2) and pancreatic (ASPC-1, PL45) cancer cell lines. CR epithelial cells were isolated from sections of normal colon mucosa from two patients using EDTA as previously described [ S. Nakamura, I. Kino, S. Baba, *Gut* **34**, 1240 (1993)]. Histopathology confirmed that the isolated cells were greater than 90% epithelial. Isolation of Poly-A RNA and SAGE was performed as previously described (2). SAGE data was analyzed by means of SAGE software and GenBank Release 95 as previously described (2).

4. A total of 69,393 different SAGE tags were identified among the 303,706 tags analyzed. A small fraction of these different tags were likely due to sequencing errors. SAGE analysis of yeast (2), wherein the entire genomic sequence is known, demonstrated a sequencing error rate of ~ 0.7%, translating to a SAGE tag error rate of 6.8% ($1 - 0.993^{10}$). Because these sequencing mistakes are essentially random, they do not substantially affect the analysis although they could artificially inflate the number of unique genes identified. Therefore, to be conservative, we reduced our estimate of unique genes identified by this maximum tag error rate (e.g., 6.8% of 303,706 total tags). The number of different tags derived from the same gene due to alternative splicing was assumed to be negligible.

5. Abundances can be simply determined by dividing the observed number of tags for a given transcript by the total number of tags obtained. An estimate of approximately 300,000 transcripts per cell was used to convert the abundances to copies per cell [N. D. Hastie, J. O. Bishop, *Cell* 9, 761 (1976)].

6. J. O. Bishop, J. G. Morton, M. Rosbash, M. Richardson, *Nature* 250, 199 (1974); B. Lewin, Gene Expression Vol 2 (John Wiley and sons, New York 1980).

7. Computer simulations indicated that analysis of 300,000 tags would yield a 92 % chance of detecting a tag for a transcript whose expression was at least three copies per cell on average among the tissues examined and assuming 300,000 transcripts per cell.

8. To minimize the number of assumptions and to account for the large number of comparisons being made, Monte Carlo analysis was used for determining statistical significance. The null hypothesis was that the level, kind, and distribution of transcripts were the same for cancer and normal cells. For each transcript, 100,000 simulations were performed to determine the relative likelihood due to chance alone ("p-chance") of obtaining a difference in expression equal to or greater than the observed difference, given the null hypothesis. This likelihood was converted to an absolute probability value by simulating 40 experiments in which a representative number of transcripts (27,993 transcripts in each experiment) was identified and compared. The distribution of transcripts used for these simulations was derived from the average level of expression observed in the original samples. The distribution of the p-chance scores obtained in the 40 simulated experiments (false positives) was then compared to those obtained experimentally. Based on this comparison, a maximum value of 0.0005 was chosen for p-chance. This yielded a false positive rate that was no higher than 0.01 for the least significant p-chance value below the cutoff.

9. Two hundred simulations assuming an abundance of 0.0001 in one sample and 0.0006 in a second sample revealed a significant difference ($P < 0.01$, [8]) 95% of the time.

10. It is not possible to obtain pancreatic ductal epithelium, from which pancreatic carcinomas arise, in sufficient quantities to perform SAGE. It is therefore not possible to determine whether these transcripts were derived from genes that were highly expressed only in pancreatic cancers or were also expressed in pancreatic duct cells.

11. Total RNA isolation and Northern blot analysis was performed as described [ W. S. el-Deiry, *et al.*, *Cell* **75**, 817 (1993)].

12. A. H. Owens, D. S. Coffey, S. B. Baylin, Eds., Tumor Cell Heterogeneity: Origins and Implications (Academic Press, New York, 1982).

13. Northern blot analyses were done on 45 of the 337 differentially expressed transcripts with tentative database matches. In three cases, the pattern of expression was not differentially expressed as predicted by SAGE and, for the purposes of this calculation, were presumed to represent incorrect database matches.

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26. In the case of normal and neoplastic colon cancer tissue, 548 differentially transcripts were identified among the 36,125 unique transcripts.

27. All references cited are hereby incorporated by reference herein.

28. Sequences tags in Tables 2-4 are consecutively numbered to form SEQ ID NOS: 1-732.

CLAIMS

1. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

identifying the first sample as neoplastic when the level of the at least one transcript is found to belower in the first sample than in the second sample.

2. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

3. The method of claim 1 wherein a comparison of at least two of said transcripts is performed.

4. The method of claim 2 wherein a comparison of at least two of said transcripts is performed.

5. The method of claim 1 wherein a comparison of at least five of said transcripts is performed.

6. The method of claim 2 wherein a comparison of at least five of said transcripts is performed.

7. The method of claim 1 wherein a comparison of at least ten of said transcripts is performed.

8. The method of claim 2 wherein a comparison of at least ten of said transcripts is performed.

9. The method of claim 1 wherein a comparison of at least twenty of said transcripts is performed.

10. The method of claim 2 wherein a comparison of at least twenty of said transcripts is performed.

11. The method of claim 1 wherein a comparison of at least thirty of said transcripts is performed.

12. The method of claim 2 wherein a comparison of at least thirty of said transcripts is performed.

13. An isolated and purified human nucleic acid molecule which comprises a SAGE tag selected from SEQ ID NO:1-732.

14. The nucleic acid molecule of claim 13 which is a cDNA molecule.

15. The nucleic acid molecule of claim 13 wherein the SAGE tag is located at the 3' end of the molecule, adjacent to the 3'-most NlaIII restriction enzyme site.

16. An isolated nucleotide probe comprising at least 10 nucleotides of a human nucleic acid molecule, wherein the human nucleic acid molecule comprises a SAGE tag selected from SEQ ID NO: 1-732.

17. The probe of claim 16 which comprises the selected SAGE tag.

18. A diagnostic reagent for evaluating neoplasia of a colorectal tissue, comprising at least 2 probes according to claim 16.

19. The diagnostic reagent of claim 18 which comprises at least 5 probes according to claim 16.

20. The diagnostic reagent of claim 18 which comprises at least 10 probes according to claim 16.

21. The diagnostic reagent of claim 18 which comprises at least 20 probes according to claim 16.

22. The diagnostic reagent of claim 18 which comprises at least 30 probes according to claim 16.

23. A diagnostic reagent for evaluating neoplasia of a colorectal tissue, comprising at least 2 probes according to claim 17.

24. A method of diagnosing pancreatic cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

25. A method of diagnosing cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue of the same tissue type, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

26. A method to aid in the determination of a prognosis for a colon cancer patient, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of the at least one transcript is found to be lower in the first sample than in the second sample.

27. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of at least one transcript in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

28. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

identifying the first sample as neoplastic when the level of expression of the protein is found to be lower in the first sample than in the second sample.

29. A method of diagnosing colon cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a colonic tissue suspected of being neoplastic and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

30. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

31. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

32. A method of diagnosing pancreatic cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of a pancreatic tissue suspected of being neoplastic and the second sample is of a normal human colon tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

33. A method of diagnosing cancer in a sample suspected of being neoplastic, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a tissue suspected of being neoplastic and the second sample is of a normal human tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

identifying the first sample as neoplastic when expression of the protein is found to be higher in the first sample than in the second sample.

34. A method to aid in the determination of a prognosis for a colon cancer patient, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic colonic tissue and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 3;

determining a poorer prognosis if the level of expression is found to be lower in the first sample than in the second sample.

35. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of expression of at least one protein in a first tissue sample to a second sample, wherein the first sample is of a colonic cancer tissue and the second sample is of a normal human colonic tissue, and wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

36. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic pancreatic tissue and the second sample is of a normal human colon tissue, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

37. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

comparing the level of expression of at least one protein in a first sample of a tissue to a second sample, wherein the first sample is of a neoplastic tissue and the second sample is of a normal human tissue of the same tissue type, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5;

determining a poorer prognosis if the level of expression is found to be higher in the first sample than in the second sample.

38. A method of treating a cancer cell, comprising the step of:

administering to a cancer cell an antibody which specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5, wherein the antibody is linked to a cytotoxic agent.

39. An antibody linked to a cytotoxic agent, wherein the antibody specifically binds to a protein encoded by a transcript identified by a tag selected from the group consisting of those shown in Tables 2, 4, and 5.

40. A method of detecting colon cancer in a patient, comprising the steps of:

comparing the level of at least one protein in a first body sample to a second body sample, wherein the first sample is a body sample of the patient and the second sample is of a normal human, wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein is found to be higher in the first sample than in the second sample.

41. A method of detecting pancreatic cancer in a patient, comprising the steps of:

comparing the level of at least one protein encoded by a transcript in a first sample of a tissue to a second sample, wherein the first sample is of the patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein is found to be higher in the first sample than in the second sample.

42. A method of detecting cancer in a patient, comprising the steps of:

comparing the level of at least one protein in a first sample to a second sample, wherein the first sample is of patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one protein is found to be higher in the first sample than in the second sample.

43. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of at least one protein in a first sample to a second sample, wherein the first sample is of a colonic cancer patient and the second sample is of a normal human, wherein the protein is encoded by a transcript identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein is found to be higher in the first sample than in the second sample.

44. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

comparing the level of at least one protein in a first sample to a second sample, wherein the first sample is of a pancreatic cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those shown Table 4, wherein said first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein is found to be higher in the first sample than in the second sample.

45. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

comparing the level of expression of at least one protein in a first sample to a second sample, wherein the first sample is of a cancer patient and the second sample is of a normal human, wherein said protein is encoded by a transcript identified by a tag selected from the group consisting of those

shown Table 5, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one protein is found to be higher in the first sample than in the second sample.

46. A method of detecting colon cancer in a patient, comprising the steps of:

comparing the level of at least one transcript in a first body sample to a second body sample, wherein the first sample is a body sample of the patient and the second sample is of a normal human, wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

47. A method of detecting pancreatic cancer in a patient, comprising the steps of:

comparing the level of at least one transcript in a first sample of a tissue to a second sample, wherein the first sample is of the patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

48. A method of detecting cancer in a patient, comprising the steps of:

comparing the level of at least one transcript in a first sample to a second sample, wherein the first sample is of patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected

from the group consisting of those shown Table 5, wherein the first and second body sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

identifying neoplasia when the level of the at least one transcript is found to be higher in the first sample than in the second sample.

49. A method to aid in determining a prognosis for a patient with colon cancer, comprising the steps of:

comparing the level of at least one transcript in a first sample to a second sample, wherein the first sample is of a colonic cancer patient and the second sample is of a normal human, wherein the transcript is identified by a tag selected from the group consisting of those shown in Table 2, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

50. A method to aid in determining a prognosis of a patient having pancreatic cancer, comprising the steps of:

comparing the level of at least one transcript in a first sample to a second sample, wherein the first sample is of a pancreatic cancer patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 4, wherein said first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

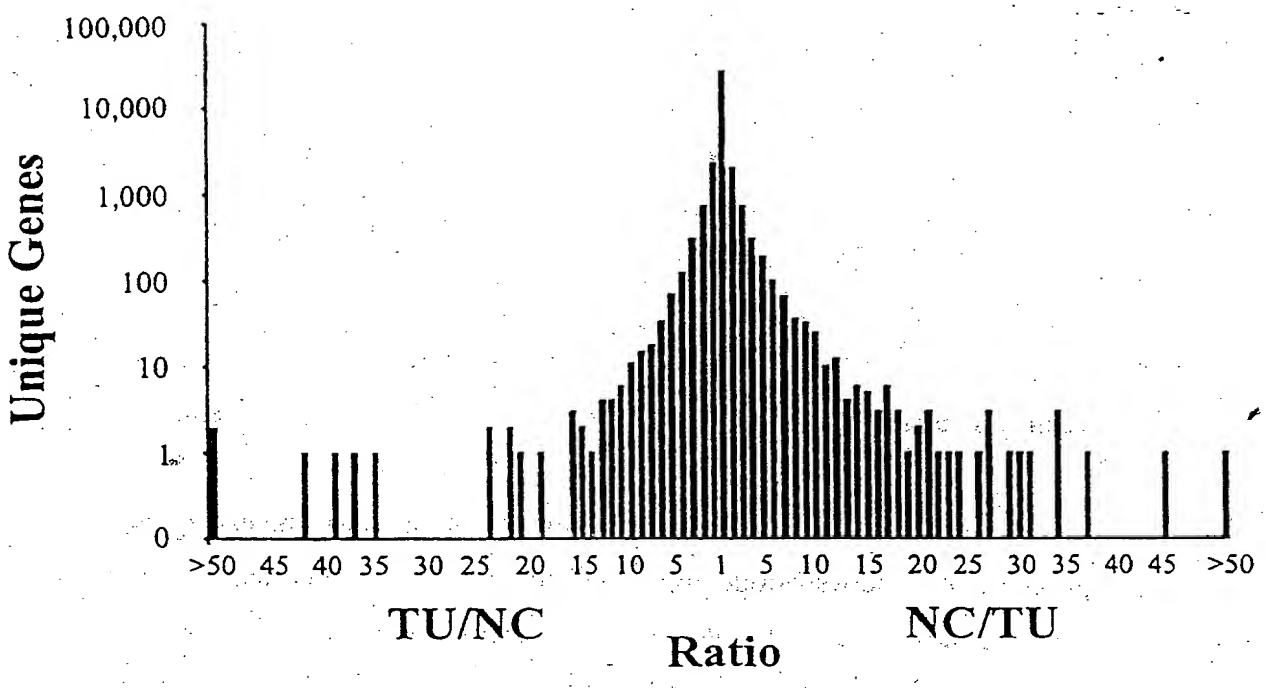
determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

51. A method to aid in providing a prognosis for a cancer patient, comprising the steps of:

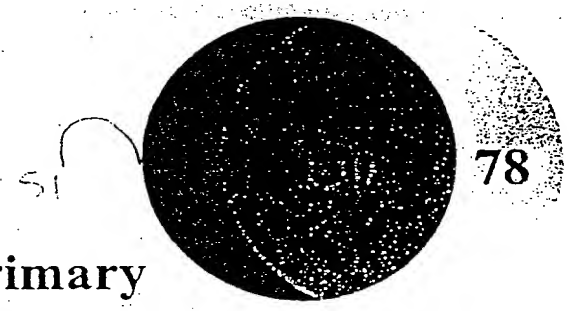
comparing the level of expression of at least one transcript in a first sample to a second sample, wherein the first sample is of a cancer patient and the second sample is of a normal human, wherein said transcript is identified by a tag selected from the group consisting of those shown Table 5, wherein the first and second sample is a sample selected from the group consisting of blood, urine, feces, sputum, and serum;

determining a poorer prognosis if the level of the at least one transcript is found to be higher in the first sample than in the second sample.

52. A method for screening for candidate agents that modulate the expression of a polynuleotide selected from the group consisting of the polynucleotides in SEQ ID NOS:1-732 or their respective complements, comprising contacting a test agent with a colon or pancreatic cell and monitoring expression of the polynucleotide, wherein the test agent which modifies the expression of the polynucleotide is a candidate agent.




B.




C.

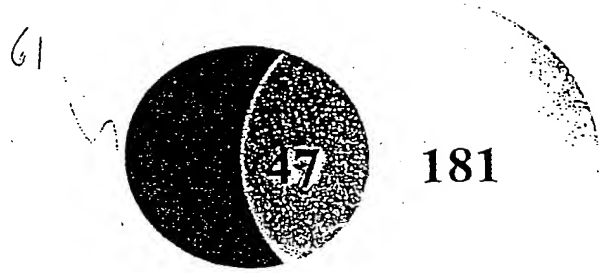


FIG. 2

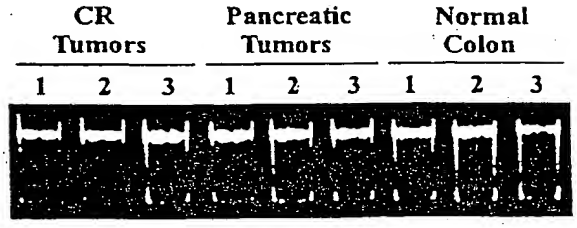
A.


| | SAGE Data | |
|---|---|---|
| | T | N |
| H204104 | 11 | 102 |
| H259108 | 1 | 37 |
| H1000193 | 56 | 12 |
| H998030 | 55 | 7 |

B.


| | SAGE Data | |
|---|---|---|
| | Pancreatic Tumors | Normal Colon |
| H294155 | 47 | 0 |
| H560056 | 32 | 0 |

C.




| | SAGE Data | | |
|---|---|---|---|
| | CR Tumors | Pancreatic Tumors | Normal Colon |
| H802810 | 27 | 0 | 1 |
| H85882 | 10 | 26 | 0 |
| H618841 | 8 | 62 | 0 |

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(54) Title: GENE EXPRESSION PROFILES IN NORMAL AND CANCER CELLS

(57) Abstract

As a step towards understanding the complex differences between normal and cancer cells, gene expression patterns were examined in gastrointestinal tumors. More than 300,000 transcripts derived from at least 45,000 different genes were analyzed. Although extensive similarity was noted between the expression profiles, more than 500 transcripts that were expressed at significantly different levels in normal and neoplastic cells were identified. These data provide insights into the extent of expression differences underlying malignancy and reveal genes that are useful as diagnostic or prognostic markers.

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# INTERNATIONAL SEARCH REPORT

Inter onal Application No
PCT/US 98/10277

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68 G01N33/574

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | SUGIO K ET AL.: "Differential expression of c-myc gene and c-fos gene in premalignant and malignant tissues." CANCER RESEARCH, vol. 48, no. 17, 1988, pages 4855-4861, XP002089885 see the whole document --- | 1,3,13, 16,17,28 |
| X | VAN BELZEN N ET AL.: "Detection of different gene expression in differentiating colon carcinoma cells by differential display" JOURNAL OF PATHOLOGY, vol. 178, no. Suppl., - 1996 page 2A XP002089886 | 1,3,5,7, 9,11 |
| Y | see abstract --- -/-- | 26,28,34 |

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Interi ·nal Application No
PCT/US 98/10277

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| Y | WO 95 21944 A (SMITHKLINE BEECHAM CORP ;ROSENBERG MARTIN (US); DEBOUCK CHRISTINE) 17 August 1995<br>see the whole document | 26,28,34 |
| Y | EP 0 284 362 A (ICI PLC) 28 September 1988<br>see abstract<br>see page 2, line 44 - line 51<br>see page 10, line 12 - line 15; claims 1,9; figure 2 | 1,3,5,7, 9,11, 13-23, 26,28, 34,52 |
| Y | EP 0 761 822 A (UNIV JOHNS HOPKINS MED) 12 March 1997<br>see the whole document | 1,3,5,7, 9,11, 13-23, 26,28, 34,52 |
| Y | WO 95 11923 A (DANA FARBER CANCER INST INC ;CHEN LAN BO (US); BAO SHIDENG (CN); L) 4 May 1995<br>see the whole document | 1,3,5,7, 9,11, 13-18, 23,26, 28,34,52 |
| Y | VELCULESCU V E ET AL: "SERIAL ANALYSIS OF GENE EXPRESSION"<br>SCIENCE,<br>vol. 270, 20 October 1995,<br>pages 484-487, XP002053721<br>cited in the application<br>see the whole document | 1,3,5,7, 9,11, 13-18, 23,26, 28,34,52 |
| Y | SCHWEINFEST C W ET AL.: "Subtraction hybridization cDNA libraries from colon carcinoma and hepatic cancer"<br>GENETIC ANALYSIS TECHNIQUES AND APPLICATIONS,<br>vol. 7, 1990,<br>pages 64-70, XP002089887<br>see the whole document | 1,3,5,7, 9,11, 13-18, 23,26 |
| Y | WO 97 14812 A (CHIRON CORP) 24 April 1997<br>see the whole document | 52 |
| A | GRESS T M ET AL.: "A pancreatic cancer-specific expression profile"<br>ONCOGENE,<br>vol. 13, 1996,<br>pages 1819-1830, XP002089888<br>see the whole document | |

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# INTERNATIONAL SEARCH REPORT

Interi nal Application No
PCT/US 98/10277

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| A | WO 95 19369 A (UNIV VANDERBILT) 20 July 1995<br>see the whole document | |
| A | GRESS T ET AL.: "Identification of genes with pancreatic cancer specific expression by use of cDNA representational difference analysis"<br>GASTROENTEROLOGY,<br>vol. 110, no. 4 Suppl., 1996, XP002089889<br>see abstract | |
| P,X | ZHANG L E AL.: "Gene expression profiles in normal and cancer cells."<br>SCIENCE,<br>vol. 276, 1997,<br>pages 1268-1272, XP002089890<br>see the whole document | 1,3,5,7, 9,11, 13-23, 26,28, 34,52 |
| P,X | VAN BELZEN N ET AL.: "A novel gene which is up-regulated during colon epithelial cell differentiation and down-regulated in colorectal neoplasms"<br>LABORATORY INVESTIGATION,<br>vol. 77, no. 1, 1997,<br>pages 85-92, XP002089891<br>see the whole document | 1,3,5,7, 9,11,13, 14, 16-18, 23,26, 28,34 |

# INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 98/ 10277

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see FURTHER INFORMATION sheet, subject 1.

**Remark on Protest**

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International Application No. PCT/ US 98/10277

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1,3,5,7,9,11,13-23,26,28,34,52 (partial)

   INVENTION 1:
   An isolated and purified human nucleic acid molecule comprising SEQ ID NO:291 of table 3 (INVENTION 1), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing colon cancer using them, and a method for screening for agents modulating the expression of such a sequence using them.

2. Claims: 1,3,5,7,9,11,13-23,26,28,34,52 (partial)

   INVENTION 2 to INVENTION 259:
   An isolated and purified human nucleic acid molecule comprising SEQ ID NO:292 of table 3 (INVENTION 2), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing colon cancer using them, and a method for screening for agents modulating the expression of such a sequence using them.

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   ...ibidem for each of the SEQ ID Nos:293 to 549 (INVENTION 3 to INVENTION 259) as specified in table 3, separately.

3. Claims: 2,4,6,8,10,12-23,27,29,35,38-40,43,46,49, 52 (partial)

   INVENTION 260 to INVENTION 549:
   An isolated and purified human nucleic acid molecule comprising SEQ ID NO:1 of table 2 (INVENTION 260), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing colon cancer using them, a method of treating a cancer cell using them, an antibody linked to a cytotoxic agent used in such a method, and a method for screening for agents modulating the expression of such a sequence using them.
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   ...ibidem for each of the SEQ ID Nos:2 to 290 (INVENTION 261 to INVENTION 549) as specified in table 2, separately.

4. Claims: 13-24,30,32,36,38,39,41,44,47,50,52 (partial)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

INVENTION 550 to INVENTION 732:
An isolated and purified human nucleic acid molecule comprising SEQ ID NO:550 of table 4 (INVENTION 550), an isolated nucleotide probe hybridizing to it, a diagnostic reagent comprising at least two of such probes, methods of diagnosing or prognosing pancreatic cancer using them, a method of treating a cancer cell using them, an antibody linked to a cytotoxic agent used in such a method, and a method for screening for agents modulating the expression of such a sequence using them.
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...ibidem for each of the SEQ ID Nos:551 to 732 (INVENTION 551 to INVENTION 732) as specified in table 4, separately.

5. Claims: 24,30,32,36,38,39,41,44,47,50 (partial)

INVENTION 733 to INVENTION 734:
Methods of diagnosing or prognosing pancreatic cancer relying on a human nucleic acid molecule comprising SEQ ID NO:733 of table 4 (INVENTION 733), a method of treating a cancer cell using it, and an antibody linked to a cytotoxic agent used in such a method.
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...ibidem for SEQ ID Nos:734 (INVENTION 734) as specified in table 4.

6. Claims: 25,31,33,37-39,42,45,48,51 (partial)

INVENTION 735 to INVENTION 870:
Methods of diagnosing or prognosing cancer relying on a human nucleic acid molecule comprising SEQ ID NO:735 of table 5 (INVENTION 735), a method of treating a cancer cell using it, and an antibody linked to a cytotoxic agent used in such a method.
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...ibidem for each of the SEQ ID Nos:736 to 870 (INVENTION 736 to INVENTION 870) as specified in table 5, separately.

# INTERNATIONAL SEARCH REPORT

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Inte. .onal Application No
PCT/US 98/10277

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